

# In vivo Monitoring of Transcriptional Dynamics After Lower-Limb Muscle Injury Enables Quantitative Classification of Healing

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## Supplementary Materials

Text S1: Transcriptional Signatures of Inflammation and Immune System Detected in Early Period

Text S2: Transcriptional Signatures Associated With Injured Muscle Tissue Extracellular Matrix

Text S3: Injured Muscle Tissue Microenvironment Regulates Existing and Invading Cellular Migration, Proliferation, Differentiation and Phenotype

Text S4: Activation of Muscle Repair Machinery

Text S5: Late Transcriptional Programs Activated in Response to Traumatic LLMI

Fig. S1. Immuno-histological analysis of muscle after cryo-injury.

Fig. S2. a) Example of reproducibility from RNA-Seq datasets. Biological replicates of *in vivo* isolated RNA samples from 24 hours after injury. Sequencing libraries were prepared from the isolated RNA and a strong correlation ( $R^2 = 0.95$ ) was observed for two representative examples. b) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 3 hour time point. c) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 10 hour time point. d) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 24 hour time point.

Fig. S3. Number of differentially expressed genes.

Fig. S4. Gene Sets Activated Early After Injury (3-24 hrs) a) Enriched KEGG pathways from differentially expressed genes for the early time points (3-24 hrs). The size of the circle corresponds to the number of significant genes with each enriched pathway. b) Heatmap of genes associated metabolism expressed in the early time period. c) Gene expression profile of Arginase 1 (Arg1), which is a molecule emitted by type 2 macrophages to balance inflammatory reactive-oxygen species present in the injured tissue. Red-Injured, Blue-Uninjured

Fig. S5. Examples of alternative splicing in immune network of genes.

Fig. S6. Genes associated with hematopoietic activation, proliferation and anti-inflammatory cytokines activated in early & middle periods.

Fig. S7. Gene sets associated with extra-cellular matrix remodeling & satellite cell activation.

Fig. S8. a) Enriched KEGG pathways from differentially expressed genes for the late time points. The size of the circle corresponds to the number of significant genes with each enriched pathway. b) Heatmaps of gene sets activated in late period categorized by function.

Fig. S9. Area plots of FDR values for Gene Annotation (GO) clusters over time. GO terms were separated into major functional categories, and the IQR was computed for the terms in each group. The grey lines indicate the 25<sup>th</sup> and 75<sup>th</sup> percentiles, red lines denote the 25% of gene FDR values, the blue line denotes the median FDR value, and the green line denotes the 75% for FDR.

Fig. S10. Pathway-level scoring results for test datasets from PCA and the timepoint signatures methods. a). Principal component analysis. b) Normalized time point signatures method applied to mean pathway expression values. Timepoint signatures for 6 test samples and a truth training sample. The green curve indicates the control sample that was misclassified by the algorithm at the pathway level. Time point signatures for the 9 time points (blue lines) as well as 6 test samples (red and green lines).

Fig. S11. Differentially expressed gene pathways in injured samples over time.

Table S1. Significant GO clusters (FDR <0.05) identified for differentially expressed genes through the DAVID annotation tool. Each tab represents the annotations derived for each timepoint, clustered by function and sorted by FDR value from most to least significant.

Table S2: KEGG pathways identified for differentially expressed genes (FDR < 0.05). Pathways are listed for each timepoint and sorted by FDR value from most to least significant.

Table S3. Significant GO clusters identified from the 168h time point that were obtained from differentially expressed genes that were determined to contribute the largest variance at that time point.

*Text S1: Transcriptional Signatures of Inflammation and Immune System Detected in Early Period*

Pro-inflammatory cytokines and chemotactic protein members: IL-1 $\beta$ , IL-6, IL-18, Tnf $\alpha$ , Osm, Ccl2, Ccr2, Cxcr2, Trem2, S100a8, FDR=2.21e-22 - GO:0034097, response to cytokine

Anti-inflammatory genes: Socs3, IL-1rn, IL-4 $\alpha$ , IL-10 $\alpha$ , IL-13 $\alpha$ 1, FDR=4.31e-10 - GO:0050728, negative regulation of inflammatory response

Invading immune cell genes: Cd68, Ly6c, Cd14, Cd163, Mrc1, Ptprc, Cd24a, Cd63, Itgam, Clec7a, Ltf, Irf7, Hp, FDR=7.6e-7 - GO:0050900, leukocyte migration involved in inflammatory response

Cytokines and chemokines: Yml, S100a9, Spp1, Ccr1, Ccl3, Ccl11, Lcn2, Cxcl5, Ccl12, FDR=3.8e-44 - GO:0001816, cytokine production, FDR=9.05e-14 - GO:0032602, chemokine production

Signaling lymphocytic activation molecule family: Slamf7, Slamf8, Ly9, FDR=3.44e-16 - GO:0046649, lymphocyte activation

Pro-apoptotic loci: Casp1, Casp4, Casp8, Apaf1, Fas, FDR=1.40e-9 - GO:2001235, positive regulation of apoptotic signaling pathway

Anti-apoptotic loci: Xiap, Birc3, Birc5, Api5, Bax, Mcl1, Bcl2l1, FDR=2.17e-23 - GO:0043066, negative regulation of apoptotic process

*Text S2: Transcriptional Signatures Associated With Injured Muscle Tissue Extracellular Matrix*

Structural components of extra-cellular matrix (ECM) remodeling: Colla1, Colla2, Col3a1, Col5a1, Col5a2, Col5a3, Col6a1, Col6a2, Col6a3, Eln, FDR=4.19e-111 - GO:0016043, cellular component organization

Connective tissue: Fbn1, Ctgf, Has1, Hbegf, Fn1, Sparc, Tnc, FDR=6.65e-14 - GO:0061448, connective tissue development

ECM cross-linking enzymes: Lox, Loxl1, Loxl2, Plod3, Leprel2, P4hb

Small leucine-rich proteoglycans: Dcn, Bgn, Kera, Vcan, Lum, Ogn, FDR=3.69e-28 - GO:0036211, protein modification process

Adhesive glycoproteins: Pcolce, Itbpbp1, Lgals1, Dpt, Postn, Emilin2, Efemp2, Igfbp7, FDR=3.36e-16 - GO:0043062, extracellular structure organization

Tgf- $\beta$  superfamily: Tgf- $\beta$ i, Tgf- $\beta$ r1, Tgf- $\beta$ r2, Tgf- $\beta$ 1

Formation and stabilization of blood vessels and arterial repair: Ang, Angpt2, Angptl1, Angptl4, Angptl7, Cthrc1, Aif1, FDR=3.12e-10 - GO:0001525, angiogenesis

Contractile fibers: ActB, Actg, Capg, Arpc3, Cotl1, Tln1, Tagln, Vcl, RhoA, FDR=7.8e-5 - GO:0030833, regulate actin filament polymerization, FDR=1.5e-3 - GO:0032273, positive regulation of protein polymerization

Integrin-associated genes: Itga5, Itga7, Itgam, Itgav, Itgb1, Itgb2, FDR=3.34e-5 - GO:0007229, integrin-mediated signaling pathway

Mmps, Adams and Timps: Mmp2, Mmp3, Mmp8, Mmp14, Mmp19, Adam8, Adam15, Adam19, Timp1, Timp2, FDR=6.83e-8 - GO:0048771, tissue remodeling

*Text S3: Injured Muscle Tissue Changes from Pro- to Anti-Inflammatory States Several Days After Injury*

Innate immunity and microbial recognition: Tlr1, Tlr7, Tlr8, FDR=0.003 - GO:0034121, regulation of toll-like receptor signaling pathway

Antigen presentation and hematopoietic activation and proliferation: Ptprc, IL-21r, IL-17ra, Vav1, Lyz2, Csf1r, Csf2rb, Csf2ra, Il3ra, Il5ra, Ifi204, Aif1, FDR=1.4e-8 - GO:0042110, T cell activation, FDR=8.18e-19 - GO:0030097, Haematopoiesis

Anti-inflammatory cytokines: IL-1rl1, Il-4ra, IL-10 $\alpha$ , Msr1, IL-13ra1, S100a9, FDR=2.9e-10 - KEGG mmu04630, cytokine-cytokine receptor interaction, FDR=9e-3 - GO:0010934, macrophage cytokine production

Phagocytic and complement cascade genes: Cyba, Ncf1, Ncf2, Ncf4, C1qa, C1qb, C1qc, C1ra, C1s, FDR=3.37e-8 - GO:0006956, complement activation, FDR=7e-6 - GO:0006909, phagocytosis

Notch signaling: Dll1, Notch2, Myc, Rbpj, Cdkn1a, FDR = 3.69e-18, GO:0002684, positive regulation of immune system process

Bone morphogenetic proteins: Bmp1, Bmp4, FDR = 0.08, GO:0005125, cytokine activity

Actively proliferating cells: Cdk1, FDR = 9.63e-9, GO:0007049, cell cycle

*Text S4: Activation of Muscle Repair Machinery*

Satellite cell markers: CD34, Itga7, Itgb1, Sdc3, Sdc4, Sdcbp, Cav1, Cxcr4, Cdh15, Ly6a, FDR=4.933e-5 - GO:0007519, muscle tissue development

Muscle-fusion genes: Tmem8c, Cdh15, Capn2, Capns1, Myof, Cav3, Itgb1, Vcam1, Itga4, FDR=2.5e-6 - GO:0098602, single organism cell adhesion

Basement membrane genes: Col4a1, Col4a2, Dysf, Trim72, Lamc2, Cav3, Ahnak, Anxa1, Anxa2, Anxa5, FDR=4.78e-9 - GO:0061024, membrane organization

Muscle-specific actins, myosins, troponins, and tropomyosins: Actl9, Clrn1, Myh3, Myl4, Myl6b, Cald1, Tpm4, Tnni1, Tnni3, Tnnt1, Tnnt2, Tnnc1, Tpm3, Des, Vim

Transcription factors: Itgb2, Rrad, Fos, JunB, FosB, Pbx2, Pbx3, Dusp5, Myc, BMyc, Mt3, Egr1, Egr2, Sgms2, Runx1, Grn, Pdlim3, Csrp3, Usf1, Arid5b, Naca, Ankrd1, Ankrd2, Atf3, Atf4, Atf6, Xbp1, Tead4, Nfe2l2, FDR=2.46e-10 - GO:0006351, transcription, DNA-templated

*Text S5: Late Transcriptional Programs Activated in Response to Traumatic LLMI*

Chemotaxis genes: Ccl6, Ccl8, Ccl9, Cxcl16, Fcrlg, Fcgr3, FDR=1.9e-5

Mast cell activation: Fyb, Fcrlg, Fcgr3, Fcgr2b, Lat2, Lcp2, FDR=3.33e-5 - GO:0045576, mast cell activation

Fc receptors: Fcrlg, Fcgr1, Fcgr3, Fcgr2b, Clec7a, Colec12, Hck, Sirpa, Slc11a1, Vav1, FDR=0.035 for KEGG mmu04664, Fc epsilon RI signaling pathway.

Lectins: Clec12a, Clec4a1, Clec4a2, Clec4a3, Clec4n, Clec7a, Clec10a.

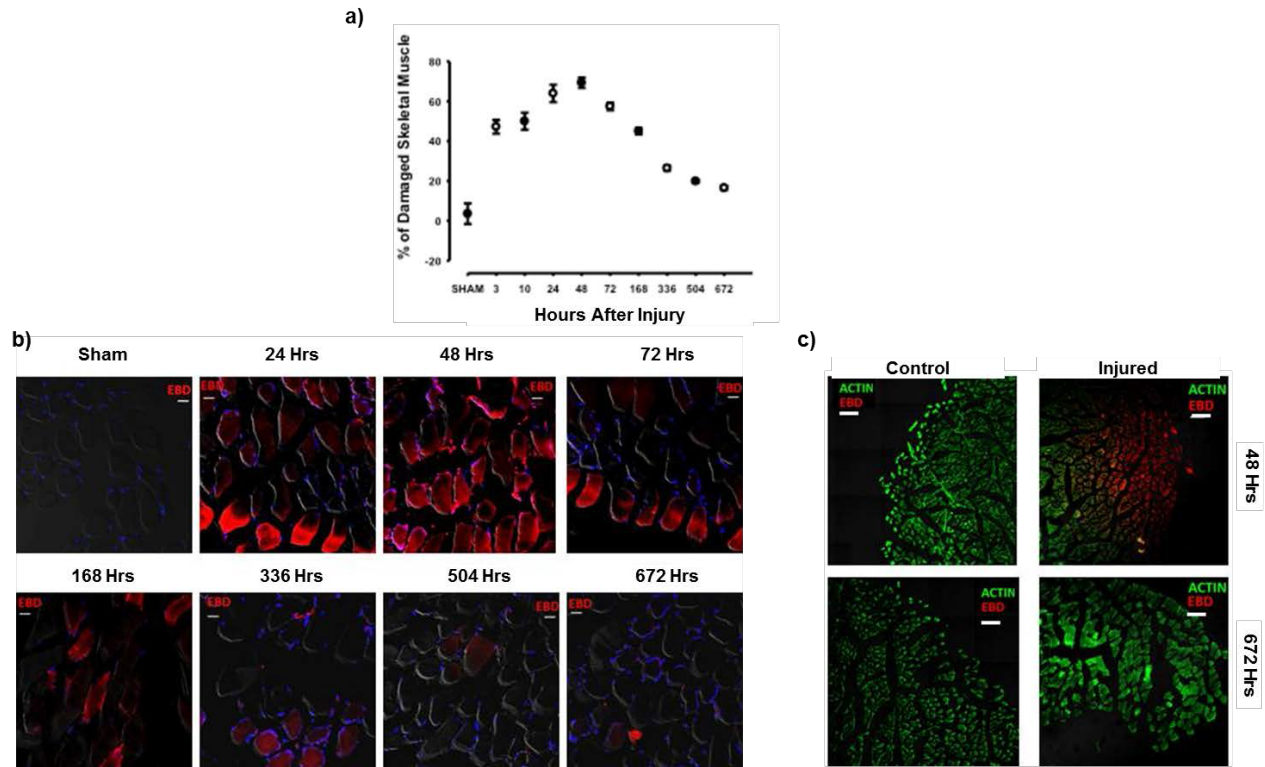
Collagen fibril organization: Adamts14, Col3a1, Col5a1, Col5a2, Dpt, Lox, and Anxa2, FDR = 1e-7)

ECM receptors: VLA proteins ( $\alpha 2$ ,  $\alpha 5$ ,  $\alpha 8$ ,  $\alpha 9$ ,  $\alpha 10$ ,  $\alpha 11$ ), cytoadhesins ( $\beta 3$ , A11- $\beta$ ), and proteoglycans (Cd44, Sdc3, Sv2), KEGG ECM-receptor interaction pathway, FDR =  $5.7e-7$

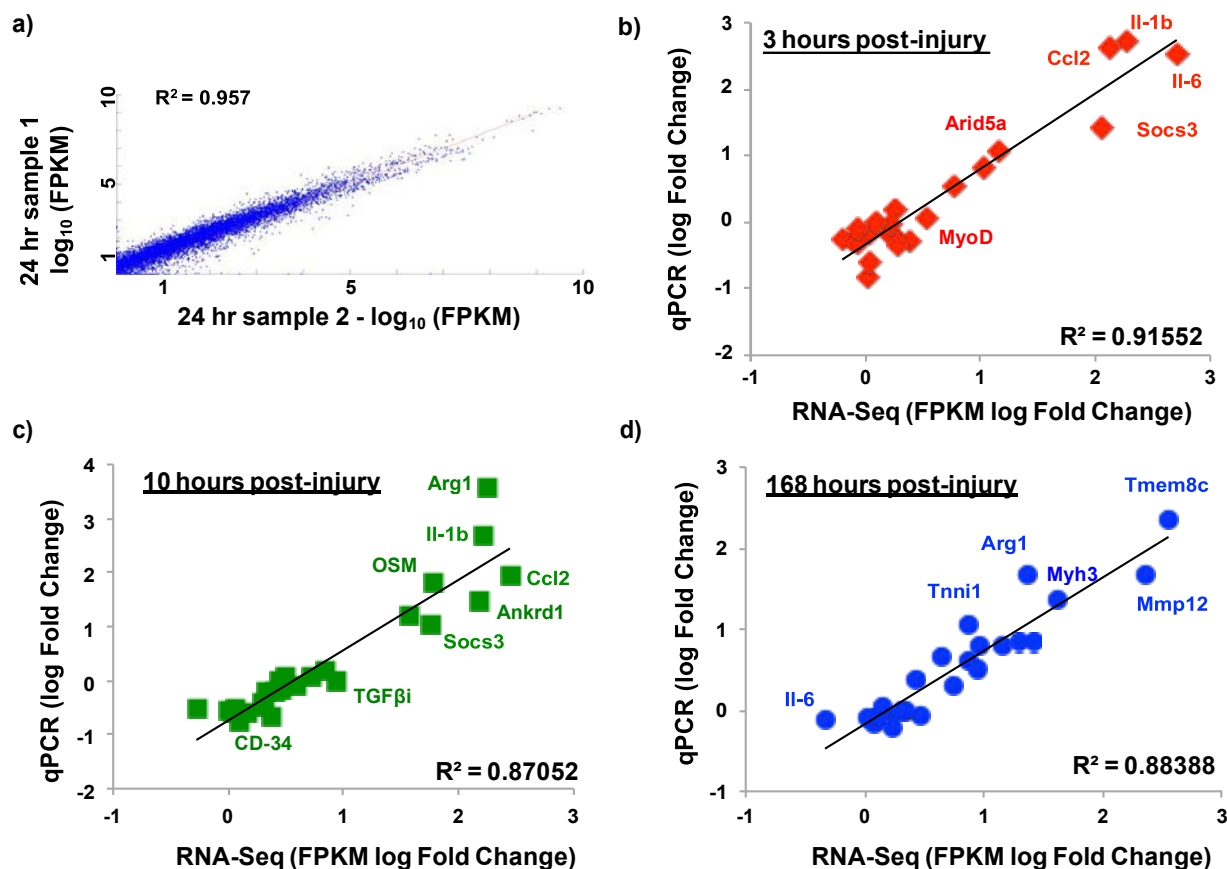
Angiogenesis genes: Col4a1, Col4a2, Robo4, Vash1, Sema5a, Sox18, GO:0001525, FDR =  $3.24e-14$

Muscle contraction and muscle system processes: Cacna1s, Myom1, Myh2, Myh4, Myh7, Nos1, Kcnma1, Ryr1, Trim63, FDR= $6.7e-4$  and  $1.6e-3$ , respectively.

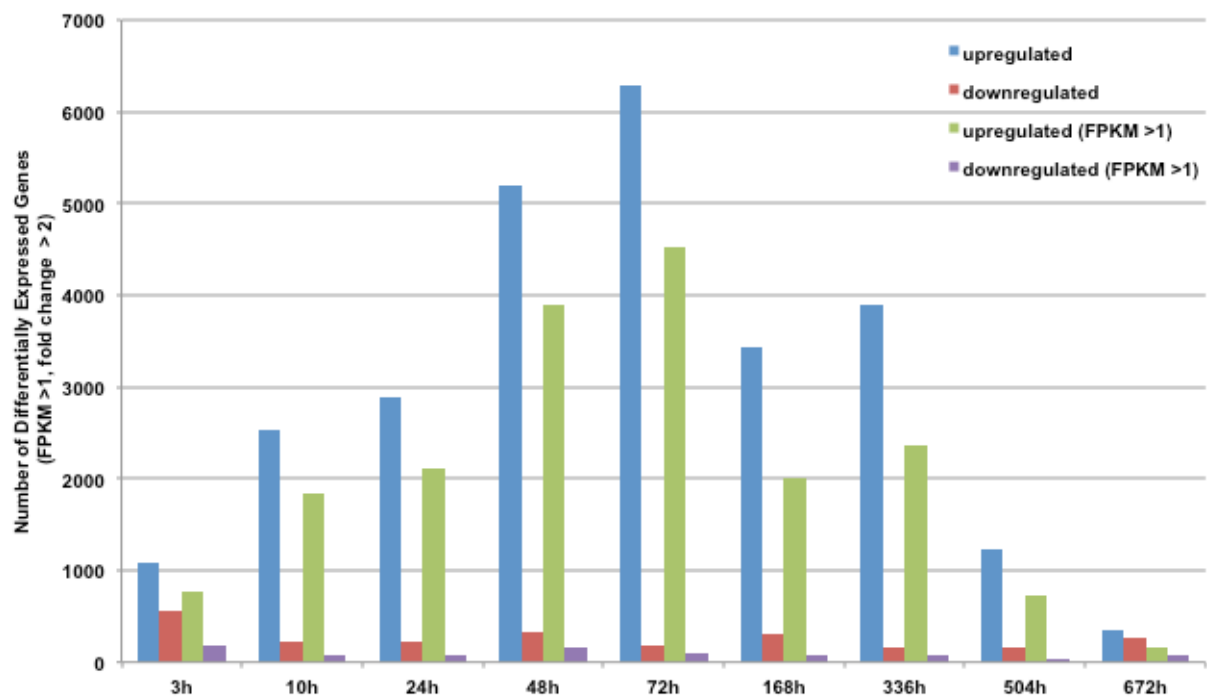
Ossification regulation: Gpnmb, Bglap, Sparc, Spp1, Runx2, Bmp1, Bmp5, Smad1



**Fig. S1.** Immuno-histological analysis of muscle after cryo-injury. a) Quantitative analysis of immuno-histological images revealed a gradual increase in tissue damage until 48 hours, indicating secondary damage to the muscle tissue occurred after the initial cryo-injury. b) Representative histological images of the injured TA stained with Evans Blue Dye (EBD – red) and DNA (blue) after several time points. c) Representative immuno-histological images at 48 hours and 672 hours after injury, whereby the green is stained for actin and red is stained for evans blue dye.

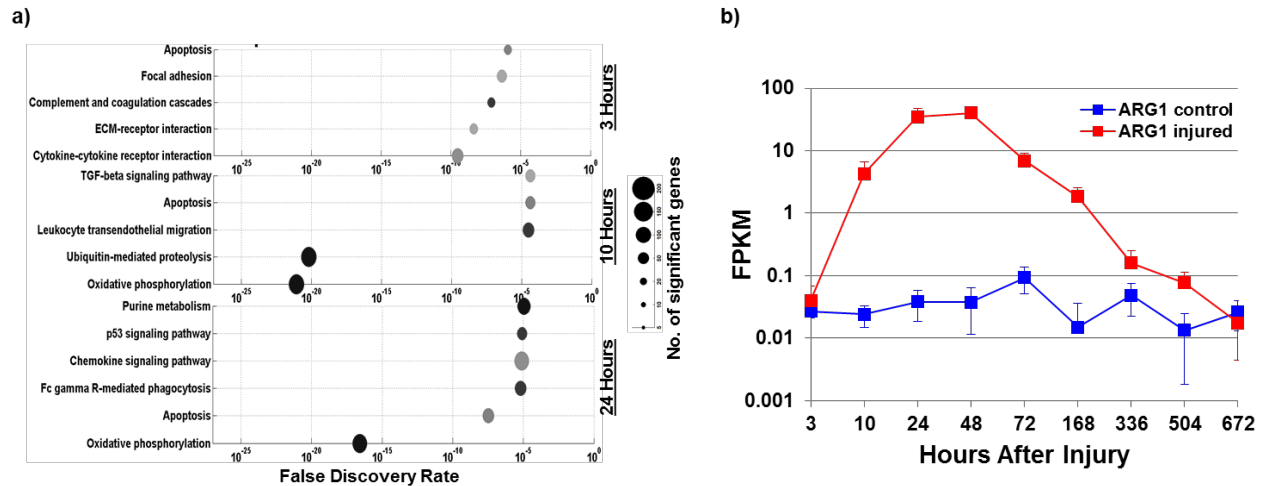


**Fig. S2.** a) Example of reproducibility from RNA-Seq datasets. Biological replicates of *in vivo* isolated RNA samples from 24 hours after injury. Sequencing libraries were prepared from the isolated RNA and a strong correlation ( $R^2 = 0.95$ ) was observed for two representative examples. b) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 3 hour time point. c) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 10 hour time point. d) Validation of RNA-Seq data with qPCR comparing the injured versus uninjured samples for the 168 hr time point.

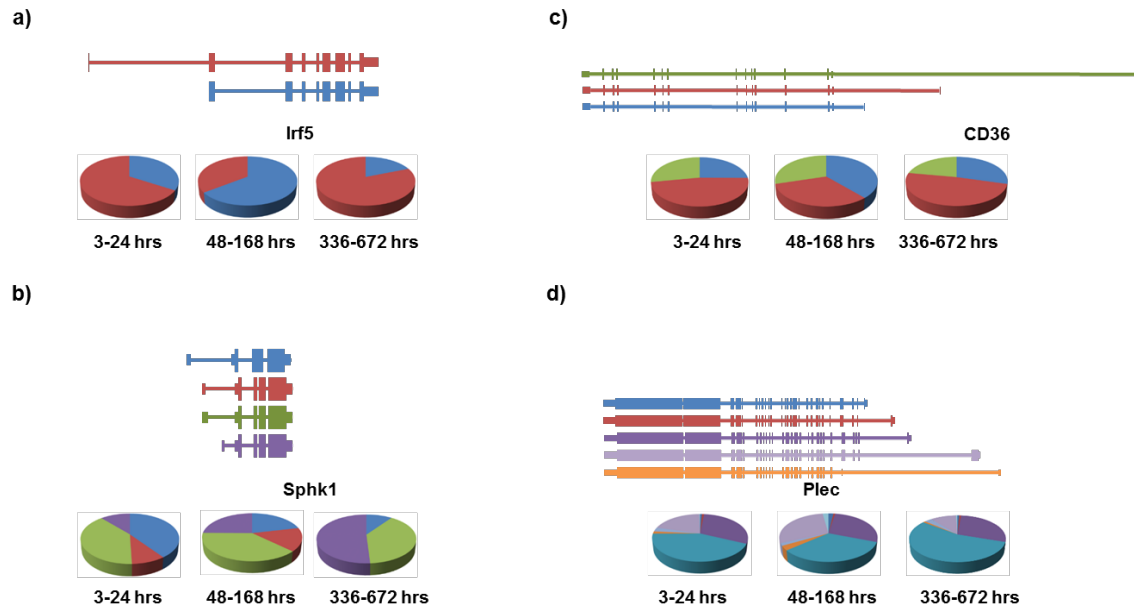


**Fig. S3.** Number of differentially expressed genes

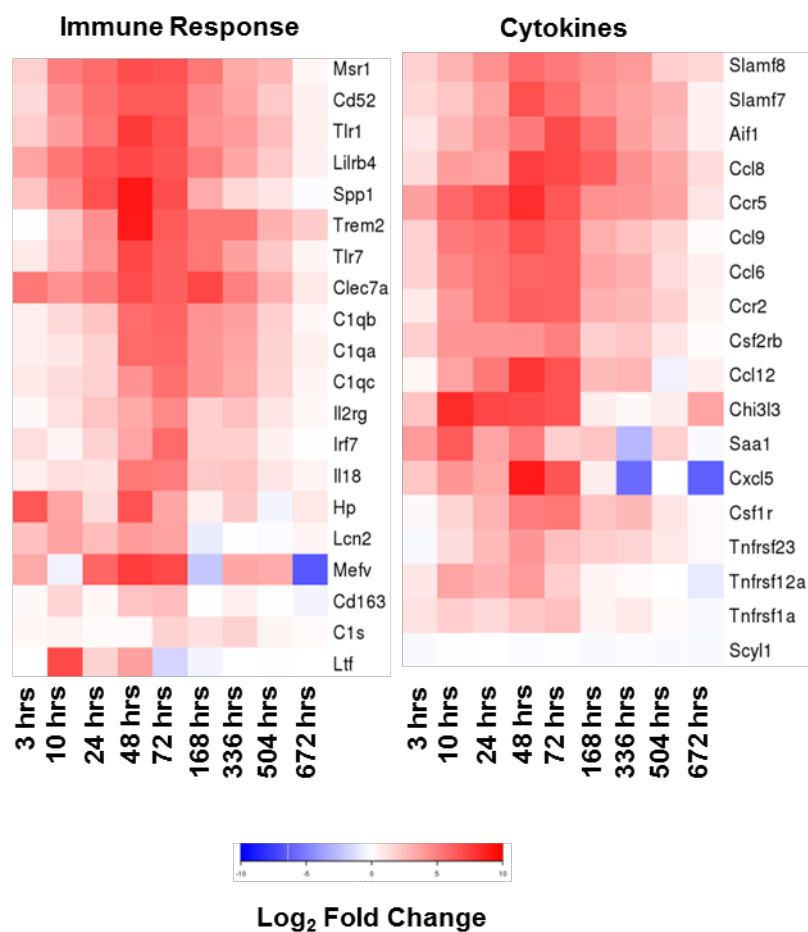




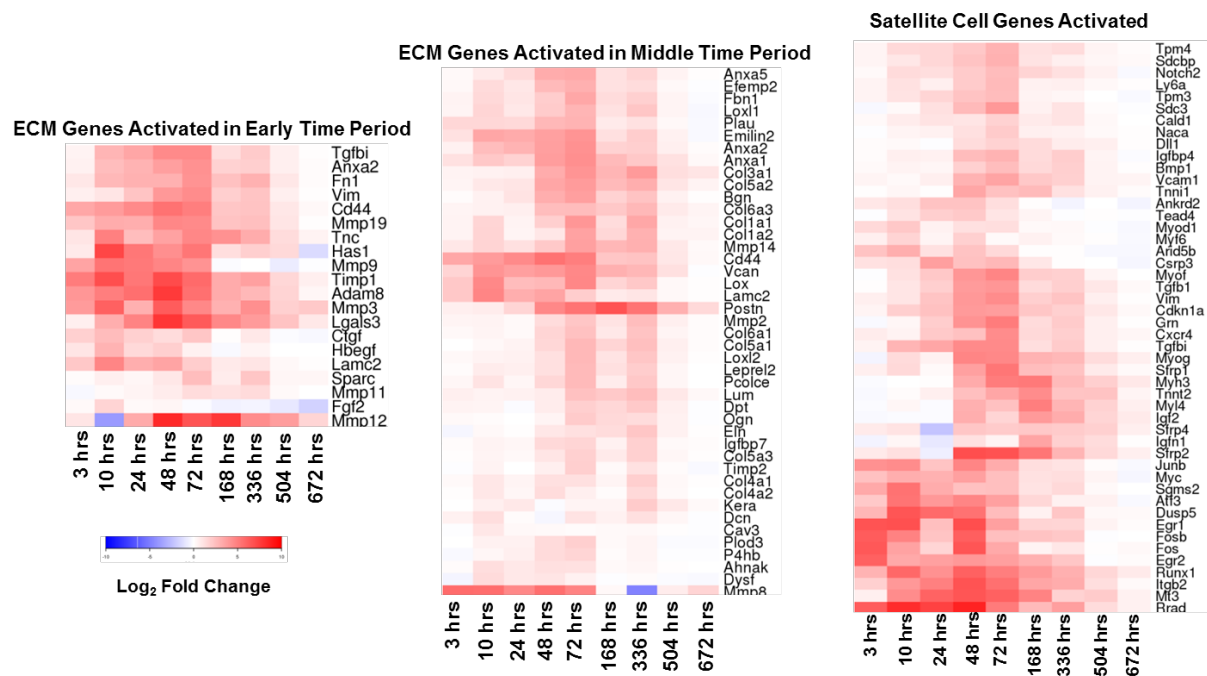
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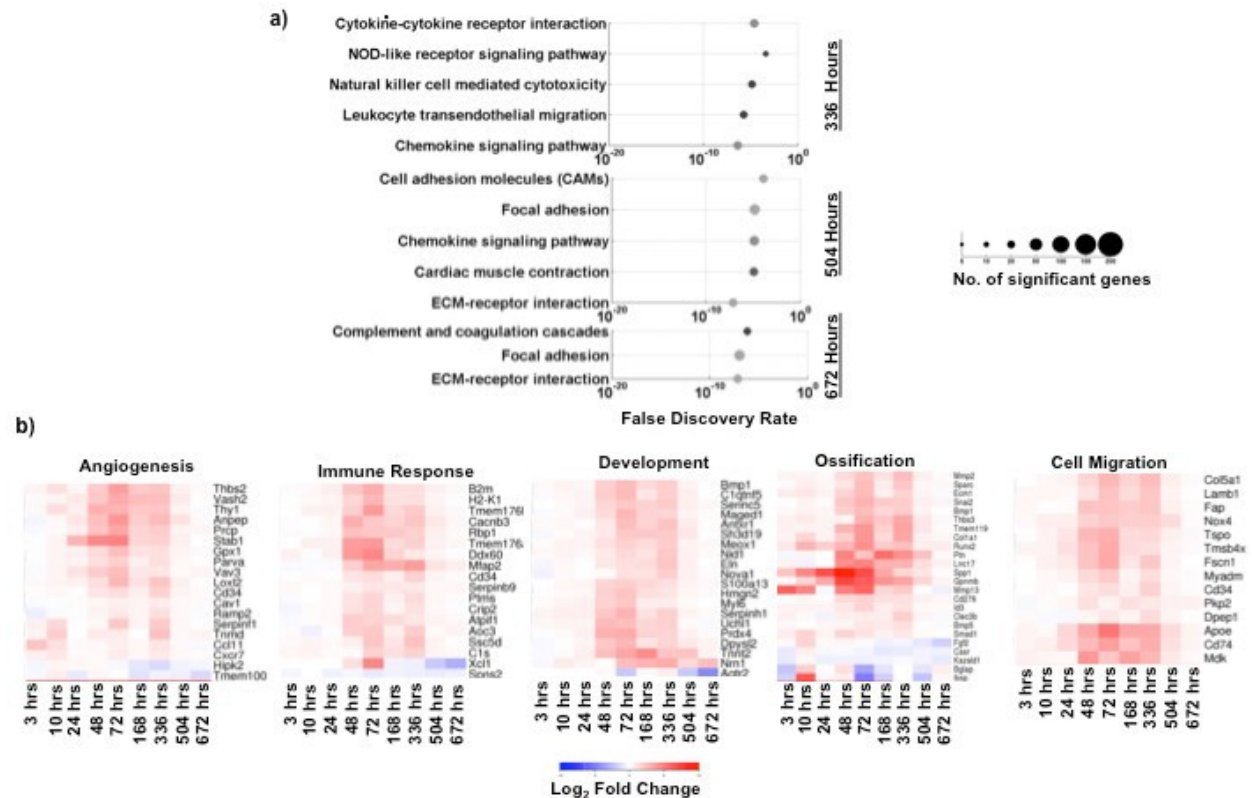
**Fig. S5.** Examples of alternative splicing in immune network of genes as determined by Cufflinks.



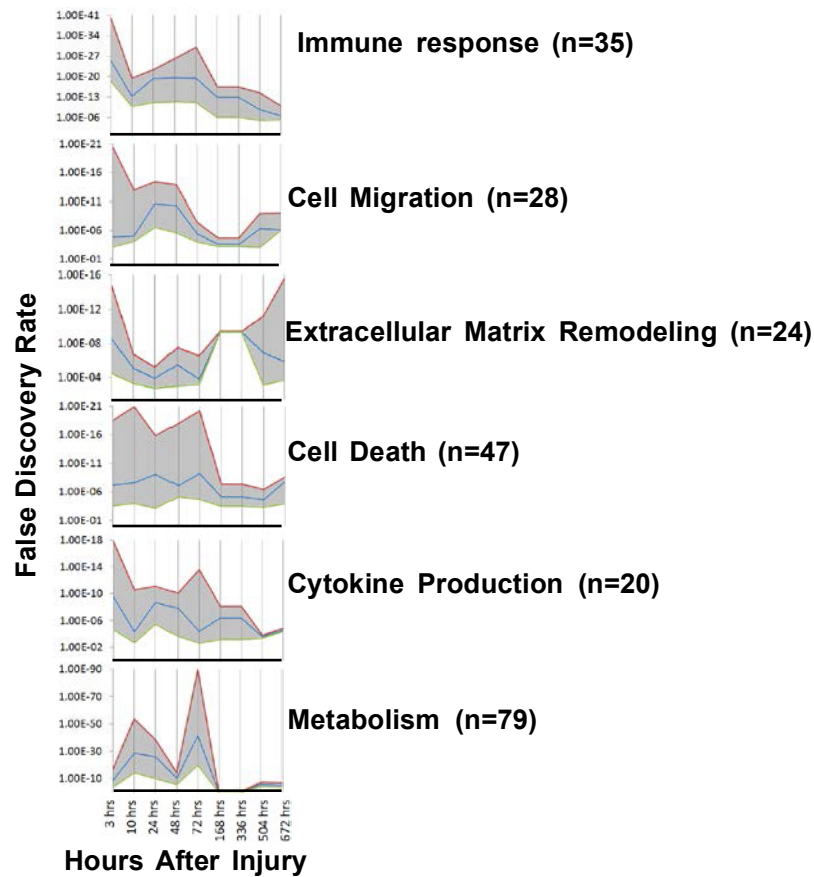
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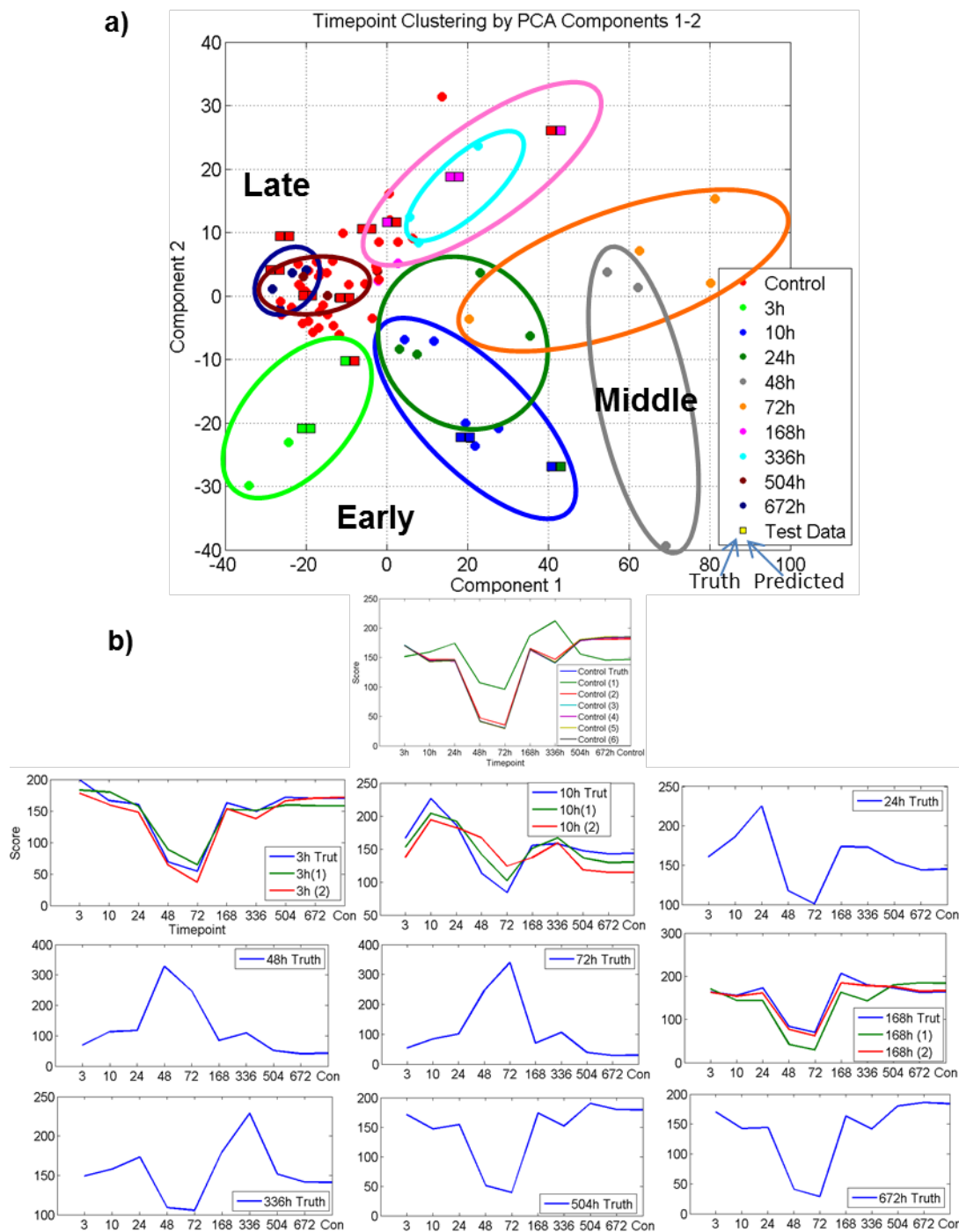
**Fig. S7.** Gene sets associated with extra-cellular matrix remodeling & satellite cell activation



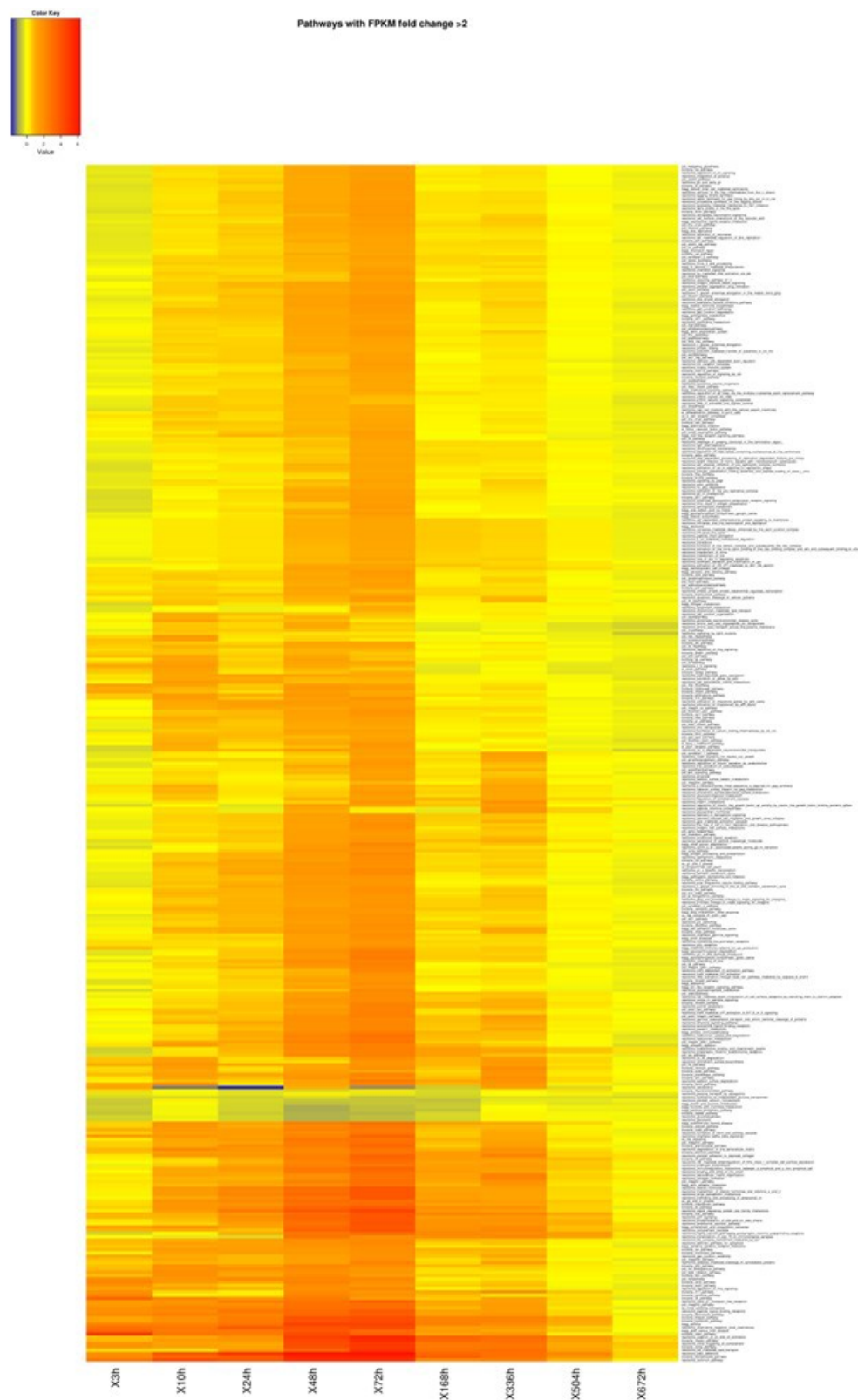
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**Fig. S10.** Pathway-level scoring results for test datasets from PCA and the timepoint signatures methods. a) Principal component analysis. b) Normalized time point signatures method applied to mean pathway expression values. The top panel represents the timepoint signatures obtained for the uninjured control datasets for 6 test samples and a truth training sample. The green curve indicates the control sample that was misclassified by the algorithm at the pathway level. The next panels are derived from time point signatures for the 9 time points (blue lines) as well as 6 test samples (red and green lines).



**Fig. S11.** Differentially expressed gene pathways in injured samples over time.







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S1.8 GO Terms upregulated 10 hours post injury													
Annotation Cluster 1	Enrichment Score: 11.839159662001325	Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
					CHN13, NRG2, F13A1, TRH1, TUR2, T18A, C1QC, TGFB1, TGFB2, CF, C19A, MYO8B, DYSE, CD44, CFH, CD, TPFG, NCF1, C4B, SERPING1, PLAUR, C1QA, C1QB, H18A, THBD, C5C5, DARIC, F3, LYST, CCR2, TPFI, CCL2, NN3J1, CCL8, ITGB2, TRIM72, CCL7, ABG1, SLC11A1, MTPN, ITGB8, ENTNP1, P1N1, PTPN6, KLF6, BMP2, CFH, TREMP2, T18J1, SPH1H2, EPHX2, CHN13, SMAD3, FGF9R, FCGR3, NCTD2, SLC7A2, CXC13, CLEC7A, HMOX1, HMOX2, PHA2, PHA2L, TOLLIP, LY86, HPA1, G1A1, CASP, SLC1A1, SNAI, PAX7, LBP, NFKB2, GAL, NLRP3, CD163, CHST1, SERPINA9, NRP9, NGR, PROS1, LCP1, PTAIR, KIM8B, CXCL1, CXCL5, C3, CXCL3, CCR1, CXCL2, PF4, ABHD2, CD244, CCL24, TNFRSF1A, ANKAR, TNFRSF3B, PYCARD, CHST1, SEIP, IL6, IL6R, ANKAS, STAT1, CCL11, CCL12, ORML1, NUPR1, BAX, HIEG, ALDOX5, 17	2080	347	13588	2.17	4.59E-13	4.59E-13	2.11E-13	
GOTERM_BP_FAT	GO:0009611"response to wounding		115	4.01	7.27E-17	BMP1B, DMG2, CD14, GDF94, TOLLIP, LY86, T18J, TUR2, T18A, C1QC, TGFB1, CF, C19A, MYO8B, CD44, SAA1, F3, LBP, CD, NFKB2, C4B, NCF1, SERPINA1, GAL, NLRP3, CD163, CHST1, C1QA, C1QB, SERPINA9, HPA1, CCR5, DAB2, CCR2, NRP9, PTAIR, ANKAR, CXCL1, CCL3, CXCL5, C3, CCR1, CXCL2, CXCL3, CXCL2, CXCL2, CD244, CCL7, CCL24, TNFRSF1A, TNFRSF1B, ITGB6, PYCARD, THBS1, P1N1, SEIP, IL6, BMP2, CFH, SPH1, T18J1, EPHX2, CHN13, SMAD3, FGF9R, STAT3, FGR3, CCL11, ORML1, CCL12, NUPR1, SLC7A2, CXCL13, ALDOX5, 19	2080	347	13588	2.17	4.59E-13	4.59E-13	2.11E-13
GOTERM_BP_FAT	GO:0006954"inflammatory response		78	2.72	1.08E-12	CLEC7A, HMOX1, BMP1B, CD14, DMG2, GDF94, BMP9, T18A, T18J, POLYR1, TUR2, T18A, C1QC, TGFB1, CF, C19A, MYO8B, CD44, CFH, CD, BCL2L1, CSAR1, NRP, NCF1, C4B, REL, SERPING1, C1QA, C1QB, H18A, C5C5, DARIC, LYST, CCR2, MAVS, IL1R1, CCL2, FGR, CCL8, ITGB2, CCL7, CD74, SLC11A1, ITGB6, FCER1G, DHX58, F1N1, PTPN6, BMP2, CARD9, CFH, IL1R1, IL1R2, T18J1, SPH1H2, EPHX2, CHN13, SMAD3, FGF9R, FCGR3, KDN1, SLC7A2, CXC13, CLEC7A, HMOX1, NRP9, BMP9, TOLLIP, LY86, H2-D1, TMEM157, SAA1, IL1AP, LBP, NFKB2, ELANE, CCL1, GAL, NLRP3, CD163, CHST1, SERPINA9, NRP9, H2-AA, PTAIR, CFSG, KIM8B, CXCL1, CXCL5, C3, CXCL1, CCR1, CXCL2, CD244, CCL24, TNFRSF1A, TNFRSF1B, PYCARD, BCL3, THBS1, PTPN6, SEIP, IL6, LY2Z, HCK, COT1L1, STAT1, CCL11, CCL12, ORML1, FGR2B, NUPR1, IFIR, APAF1, ALDOX5, BMP1B, 18	2080	225	13588	2.26	4.45E-09	2.23E-09	2.01E-09
GOTERM_BP_FAT	GO:0006952"defense response		113	3.94	3.88E-08	GMR2, CD14, GDF94, 18	2080	448	13588	1.65	1.60E-04	1.23E-05	7.23E-05
Annotation Cluster 2	Enrichment Score: 6.921603726499316	Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
					HSID17B2, POLYR1, CCL8, POSTN, FSTL1, PFA, DCK, VIT, ABISBP, ITGAM, CCL7, CD44, CTGF, COMP, CFH, ITF, PTX3, THBS1, GPNMB, FGF2, THBS2, CYR61, P1N1, BMP4, PTPRC, TNXB, PRG4, FBN1, ELANE, CHN13, STAB2, TNAGLI, PCOLCE2, VEGFA, TNFAIP6, LYVE1, EGFAM, BGN, ADAMT58, LAYN, VEGFA, HIEG, VCAN, ADAMT51, LAMC2, CLEC7A, CTSG	2006	128	13288	2.43	6.04E-06	2.01E-06	7.03E-06	
GOTERM_MF_FAT	GO:0001871"pattern binding		47	1.64	4.26E-09	HSID17B2, POLYR1, CCL8, POSTN, FSTL1, PFA, DCK, VIT, ABISBP, ITGAM, CCL7, CD44, CTGF, COMP, CFH, ITF, PTX3, THBS1, GPNMB, FGF2, THBS2, CYR61, P1N1, BMP4, PTPRC, TNXB, PRG4, FBN1, ELANE, CHN13, STAB2, TNAGLI, PCOLCE2, VEGFA, TNFAIP6, LYVE1, EGFAM, BGN, ADAMT58, LAYN, VEGFA, HIEG, VCAN, ADAMT51, LAMC2, CLEC7A, CTSG	2006	128	13288	2.43	6.04E-06	2.01E-06	7.03E-06
GOTERM_MF_FAT	GO:0030247"polysaccharide binding		47	1.64	4.26E-09	HSID17B2, POLYR1, CCL8, POSTN, PFA, FSTL1, DCK, VIT, ITGAM, ABISBP, CCL7, CD44, CTGF, COMP, CFH, ITF, THBS1, GPNMB, FGF2, THBS2, CYR61, FBN1, BMP4, PTPRC, TNXB, ELANE, STAB2, PCOLCE2, VEGFA, TNFAIP6, LYVE1, EGFAM, BGN, ADAMT58, LAYN, VEGFA, HIEG, VCAN, LAMC2, ADAMT51, 19	2006	128	13288	2.43	6.04E-06	2.01E-06	7.03E-06
GOTERM_MF_FAT	GO:0005539"glycosaminoglycan binding		41	1.43	9.18E-08	CTSG, CD209A, POLYR1, FSTL1, POSTN, CD209D, CD44, CTGF, CFH, CLEC4A1, ITF, CLEC4A2, FGF2, CYR61, ATRNL1, WSC17, PRG4, ELANE, COLEC12, CLEC4N, PCOLCE2, VEGFA, MAN2A1, TNFAIP6, EGFAM, ADAMT58, BGN, CLEC12A, C3D1, VEGFA, LAMC2, ADAMT51, VCAN, STRO1, CLEC7A, CTSG, SGLCE, GALNT7, CD248, HSID17B2, GALNT4, CCL8, PFA, DCK, VIT, CLEC10A, CD244, ITGAM, CCL7, ABISBP, GALM, COMP, GPNMB, THBS1, PTX3, SELFG, THBS2, P1N1, MRC1, BMP4, PTPRC, SEIP, TNXB, LGA33, SELL, LGA51A, FBN1, CHN13, STAB2, TNAGLI, CLEC11A, LGA51A, LVE1, GCL, LYCN, CLEC3A, GPF72, 20	2006	114	13288	2.38	1.30E-04	2.60E-05	1.51E-04
GOTERM_MF_FAT	GO:0030246"carbohydrate binding		80	2.79	2.57E-06	HIEG, CLEC7A, CYR61, CLEC4A, 20	2006	317	13288	1.67	3.63E-03	2.60E-04	4.24E-03
GOTERM_MF_FAT	GO:0008201"hexamine binding		30	1.05	5.76E-06	HSID17B2, CCL8, POSTN, PFA, FSTL1, CCL7, ITGAM, ABISBP, CTGF, COMP, CFH, ITF, GPNMB, THBS1, FGF2, THBS2, CYR61, P1N1, BMP4, PTPRC, TNXB, ELANE, PCOLCE2, VEGFA, ADAMT58, VEGFA, HIEG, LAMC2, ADAMT51, CTSG	2006	83	13288	2.39	8.12E-03	5.10E-04	9.50E-03
Annotation Cluster 3	Enrichment Score: 6.534967767280406	Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
					RHOI, ENAH, LMNA, PDGFR, JUNAK2, PDGFA, AF1, BCAR1, S100A9, POU1F1, ACTG1, GSN, CAP1, PLS3, RHOD, FANL1, ACTNA, RHO2C, PRKC1, ACTN1, TMEM180, MYH9, PANC, SIRA, WAS, FLNA, VAMP, NMR2, NMRP1, CFL1, APA2P, DBN1, LCP1, MYO5A, SHROOM3, MYL2, TCAP, CNH3, MYO9B, DAAAM1, ITGB1, EZR, RAC2, FAT1, SH2B2, BCL6, CNN2, WIPF1, CNN1, ACTC1, TNXB, GAST, CORO1C, NRAS, CORO1A, 1	2080	176	13588	2.23	4.89E-06	6.11E-07	2.21E-06	
GOTERM_BP_FAT	GO:0030029"actin filament-based process		60	2.09	1.18E-09	RHOI, ENAH, LMNA, PDGFR, JUNAK2, PDGFA, AF1, BCAR1, S100A9, POU1F1, ACTG1, GSN, CAP1, PLS3, RHOD, FANL1, ACTNA, RHO2C, PRKC1, ACTN1, TMEM180, MYH9, SIRA, WAS, FLNA, MMR2, NMRP1, CFL1, APA2P, DBN1, LCP1, SHROOM3, MYL2, TCAP, CNH3, DAAAM1, ITGB1, EZR, RAC2, FAT1, SH2B2, BCL6, CNN2, CNN1, ACTC1, TNXB, GAST, CORO1C, NRAS, CORO1A, EPB4111, EFPS, MYH11, AB12, 2	2080	176	13588	2.23	4.89E-06	6.11E-07	2.21E-06
GOTERM_BP_FAT	GO:0030030"actin cytoskeleton organization		56	1.95	5.40E-09	DAA1P, 2	2006	165	13288	2.22	2.23E-05	2.23E-06	1.01E-05
GOTERM_BP_FAT	GO:0007015"actin filament organization		24	0.84	2.92E-06	LMNA1, ACTC1, ENAH, ACTNA, AF1, BCAR1, POU1F1, PRKC1, ACTN1, GAST, SIRA, WAS, FLNA, CORO1A, EZR, GSN, CFL1, APA2P, DBN1, LCP1, PLS3, DAA1P, 1	2008	56	13588	2.80	1.20E-02	3.01E-04	5.44E-03
Annotation Cluster 4	Enrichment Score: 6.49804298543319	Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
					MAP3K8, VPS4, DHX33, PTBP2, MAP2K6, DHX32, GBS, MAGI1, ROKC2, MYLK4, GBP9, PTBP1, SPAG1, MYH7, GIM, MYH3, GILU, MAPK8, ARSEA, MAPK7, EF2AK3, EF2AK4, GNAI3, MYEF3, HSPA9A, ARFE, HSPA1B, MYT5, MYC3E, RAC2, PABPC1, DHX38, DHX9, TGFBR1, SREB1, UBE2L, ACACB, NUPR1, KCHN1, ARF1, ARF4, PRKCI, RAD542, TNK2, ACAD11, ACAD10, JUNAK2, ATP10A, ADCY1, SLC22A4, EF2K, GUCY1A3, SLC22A5, SKI1, RAP2B, SRPK2, RAP2A, AIFM2, LYN, AIFM1, PKDC2, 1700017805RUC, NOU1AD, BBS10, MAST3, SGLT, RPK1, EFPA1, ARAC, RAD30, ADH18A1, UGDH, HK1, SFR3A, ACSL1, DGKE, SNNK, PARS2, FMO2, PTX2B, CMT2, FGF9, RTR, TW2, RPS6KC1, ATP1A, BMP2K, RNF1, GAS1A, LRK1, SRXN1, HNRNAT1, ARCAQ, FGF, TRAF1, ARCA2, ZFYR5, DDXK1, HNRN1, TFC, TP53, ARCB3, RAB8B, MYO1E, MET, MYO1D, MYO1G, MYO1F, DCKC7, DCKC2, IDH3A, HKKE, ZP8K4, DCK56, ZP8K6, PUK3, PLX2, PRKAR1B, PRKAR1A, NUDF2, MYH11, AB12, RHO1, KIF22, VARS2, ATL3, SIFN8, CAD, PPK13A, FES, SIFN4, SIFN1, SIFN2, LACE1, RHOC, TET1, RHOD, ACADCA, ADCYL, ACACB, ERAL1, ACADL, NCL, ACAD9, TOR2A, ATP10A, UBE1B, RAS2, TENDL1, BTAF1, PGLI, ASNA1, HIF1A, HSPA2, ADH18A1, CHOL, HSPA5, EHDI, DCK1, EHDI, NOKA, AMR12, AP2, RHO, ABCABA, GRSF1, DACH1, VEGF, HSP90B1, GCK, DADH2, JAK1, ZRANB1, APAF1, PPK, H2-DMA, ADCY4, FASTKD1, ADCY7, U2AF2, AUKRA, PPK2, 2100057702RUC, PPKX, SUT1A3, GAS2, DALL1, GNAH41, DDD10, MPR39, RAD20, RBC1, SUGL1, PGLI, PINK1, NAV1, WNG2, PRKACCB1, CANNL1, RPS3, RHO1, RHO2, ABCBA, ACAP1, DLD, PDGFR4, MOH1, FUS, S403AS322RUC, CHA, CCLN1, PFYB8, PFYB3, FARS2, PFYB2, PFYB1, 1	2080	2183	13288	1.30	4.58E-07	4.58E-07	5.34E-07	
GOTERM_MF_FAT	GO:0000166"nucleotide site		428	14.91	3.23E-10	STK17B, MYO8B, IGFBP2, CHEK2, OAS2, IDH1, SUPV3L1, POLQ, MDC11, TRO, TREX1, ATP13A3, ATP13A5, EPHA2, HYOU1, ATP2A2, ATP2A3, NTRK2, GRS, SLC7A71, STEAP4, ACVIL1, CYBB2, CPB1B, CAMKK2, CAMKK3, CKB, ACTB3, TUBB3, TUBB8, NDC1, NTRK2, CHN13, RHO1, RHO2, ABCBA, ACAP1, DLD, PDGFR4, ARSEA, MAPK7, EF2AK3, S403AS322RUC, CHA, CCLN1, PFYB8, PFYB3, FARS2, PFYB2, PFYB1, 1	2006	1871	13288	1.31	3.91E-06	1.95E-06	4.55E-06
GOTERM_MF_FAT	GO:0017076"purine nucleotide binding		370	12.89	2.76E-09	DCKL1, EHDI, NOKA, AMR12, ACTB, ALPK2, MAPK8, RHO, ABCABA, HSP90B1, CYBB, GSK, ATP2A2, CERK, SPATAS, ETFA, AC3L5, MYO5C, CINC1A1, ACTC1, NOS1, RHO22, SWAP70, PKA4, AXL, ACV1, NADK, MAP1F1, ATP1A1, NMR2B, RPS3B2, RAD32, NIKAS, RAB1, RPS3A1, RAB30, RPS3A2, ACVY, RAB3A, GDSK, GYK, ACAS, KATNAL2, GNA13, GRIFFL2, RNASEL, DISC1, CMK1, CMK2, CMK3, CMK4, CMK5, CMK6, CMK7, CMK8, CMK9, CMK10, CMK11, CMK12, CMK13, CMK14, CMK15, CMK16, CMK17, CMK18, CMK19, CMK20, CMK21, CMK22, CMK23, CMK24, CMK25, CMK26, CMK27, CMK28, CMK29, CMK30, CMK31, CMK32, CMK33, CMK34, CMK35, CMK36, CMK37, CMK38, CMK39, CMK40, CMK41, CMK42, CMK43, CMK44, CMK45, CMK46, CMK47, CMK48, CMK49, CMK50, CMK51, CMK52, CMK53, CMK54, CMK55, CMK56, CMK57, CMK58, CMK59, CMK60, CMK61, CMK62, CMK63, CMK64, CMK65, CMK66, CMK67, CMK68, CMK69, CMK70, CMK71, CMK72, CMK73, CMK74, CMK75, CMK76, CMK77, CMK78, CMK79, CMK80, CMK81, CMK82, CMK83, CMK84, CMK85, CMK86, CMK87, CMK88, CMK89, CMK90, CMK91, CMK92, CMK93, CMK94, CMK95, CMK96, CMK97, CMK98, CMK99, CMK100, CMK101, CMK102, CMK103, CMK104, CMK105, CMK106, CMK107, CMK108, CMK109, CMK110, CMK111, CMK112, CMK113, CMK114, CMK115, CMK116, CMK117, CMK118, CMK119, CMK120, CMK121, CMK122, CMK123, CMK124, CMK125, CMK126, CMK127, CMK128, CMK129, CMK130, CMK131, CMK132, CMK133, CMK134, CMK135, CMK136, CMK137, CMK138, CMK139, CMK140, CMK141, CMK142, CMK143, CMK144, CMK145, CMK146, CMK147, CMK148, CMK149, CMK150, CMK151, CMK152, CMK153, CMK154, CMK155, CMK156, CMK157, CMK158, CMK159, CMK160, CMK161, CMK162, CMK163, CMK164, CMK165, CMK166, CMK167, CMK168, CMK169, CMK170, CMK171, CMK172, CMK173, CMK174, CMK175, CMK176, CMK177, CMK178, CMK179, CMK180, CMK181, CMK182, CMK183, CMK184, CMK185, CMK186, CMK187, CMK188, CMK189, CMK190, CMK191, CMK192, CMK193, CMK194, CMK195, CMK196, CMK197, CMK198, CMK199, CMK200, CMK201, CMK202, CMK203, CMK204, CMK205, CMK206, CMK207, CMK208, CMK209, CMK210, CMK211, CMK212, CMK213, CMK214, CMK215, CMK216, CMK217, CMK218, CMK219, CMK220, CMK221, CMK222, CMK223, CMK224, CMK225, CMK226, CMK227, CMK228, CMK229, CMK230, CMK231, CMK232, CMK233, CMK234, CMK235, CMK236, CMK237, CMK238, CMK239, CMK240, CMK241, CMK242, CMK243, CMK244, CMK245, CMK246, CMK247, CMK248, CMK249, CMK250, CMK251, CMK252, CMK253, CMK254, CMK255, CMK256, CMK257, CMK258, CMK259, CMK260, CMK261, CMK262, CMK263, CMK264, CMK265, CMK266, CMK267, CMK268, CMK269, CMK270, CMK271, CMK272, CMK273, CMK274, CMK275, CMK276, CMK277, CMK278, CMK279, CMK280, CMK281, CMK282, CMK283, CMK284, CMK285, CMK286, CMK287, CMK288, CMK289, CMK290, CMK291, CMK292, CMK293, CMK294, CMK295, CMK296, CMK297, CMK298, CMK299, CMK300, CMK301, CMK302, CMK303, CMK304, CMK305, CMK306, CMK307, CMK308, CMK309, CMK310, CMK311, CMK312, CMK313, CMK314, CMK315, CMK316, CMK317, CMK318, CMK319, CMK320, CMK321, CMK322, CMK323, CMK324, CMK325, CMK326, CMK327, CMK328, CMK329, CMK330, CMK331, CMK332, CMK333, CMK334, CMK335, CMK336, CMK337, CMK338, CMK339, CMK340, CMK341, CMK342, CMK343, CMK344, CMK345, CMK346, CMK347, CMK348, CMK349, CMK350, CMK351, CMK352, CMK353, CMK354, CMK355, CMK356, CMK357, CMK358, CMK359, CMK360, CMK361, CMK362, CMK363, CMK364, CMK365, CMK366, CMK367, CMK368, CMK369, CMK370, CMK371, CMK372, CMK373, CMK374, CMK375, CMK376, CMK377, CMK378, CMK379, CMK380, CMK381, CMK382, CMK383, CMK384, CMK385, CMK386, CMK387, CMK388, CMK389, CMK390, CMK391, CMK392, CMK393, CMK394, CMK395, CMK396, CMK397, CMK398, CMK399, CMK400, CMK401, CMK402, CMK403, CMK404, CMK405, CMK406, CMK407, CMK408, CMK409, CMK410, CMK411, CMK412, CMK413, CMK414, CMK415, CMK416, CMK417, CMK418, CMK419, CMK420, CMK421, CMK422, CMK423, CMK424, CMK425, CMK426, CMK427, CMK428, CMK429, CMK430, CMK431, CMK432, CMK433, CMK434, CMK435, CMK436, CMK437, CMK438, CMK439, CMK440, CMK441, CMK442, CMK443, CMK444, CMK445, CMK446, CMK447, CMK448, CMK449, CMK450, CMK451, CMK452, CMK453, CMK454, CMK455, CMK456, CMK457, CMK458, CMK459, CMK460, CMK461, CMK462, CMK463, 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[illegible]

[illegible]

[illegible]

						MYOD1, THRB, TGFB3, TLR2, TLR4, PNP, TGFB1, CTGTD, KDM1A, MYO8B, TRNP3, RARA, RARB, BC10, RLA, SIZ2, ARNT1, SIK4, MED13, PPARGC1B, PTHLH, HXD09, HF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NEF2L2, FUS, HMG2R, ADORA2B, CYYL1, SOX4, ITGB2, SP1, SOX9, PLAGL1, SLC11A1, TADA, AGRN, RUNX1, RUNX2, TRPS3, BMP4, KLF5, KLF6, BMP2, ESRRB, EPAS1, IZ2F1, MAFA, MAMLI1, SMDA3, CEBPB, NR4A2, ESRG, NR4A1, SMDA3, SMDA1, NR4A3, KLF15, TADA3, SREBF2, ATFA, SALLA, EAF1, CSRP1, KLF2, KLF4, PPARG, CHURCH1, FOXK1, ELFA, FOS, SDRP, GUCY1A3, YAP1, MYC, FGFR2, RHOG, SERTAD1, EGR1, AR, EGR2, HSP90AA1, TOPORS, HMGAI1, SMO, MURC, CANDI, FOXK1, INGS, ABLIM2, GLI2, ARLIM3, NUPP1, PRDM16, TNFRSF1A, REL, NFAT5, BCL3, MYOG, P753, CEBPA, BCDHA, MYT6, PER1, SMZ, ETV3, CEBPA, IL6, CEBPB, CEBPD, TBK1, AFF1, STAT1, IRF8, IRF1, PRX1, RBM14, RBM15, NFIA, ARAP1	2080	526	13588	1.50	9.57E-03	2.67E-04	4.34E-03
GOTERM_BP_FAT	GO:0051173	positive regulation of nitrogen compound metabolic process	121	4.22	2.53E-06	MYOD1, THRB, TGFB3, TLR2, TLR4, PNP, TGFB1, CTGTD, KDM1A, FOS, MYO8B, SDRP, TRNP3, RARA, YAP1, RARB, FGFR2, MYC, EGR1, AR, EGR2, SIZ2, ARNT1, SIK4, MED13, PPARGC1B, HXD09, SMO, MURC, HF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, CANDI, FOXK1, FUS, ABLIM2, HMG2R, ABLIM3, CYYL1, SOX4, NUPP1, SOX9, PLAGL1, SLC11A1, TNFRSF1A, TADA, NFAT5, BCL3, MYOG, AGRN, RUNX1, RUNX2, BMP4, CEBPA, TRPS3, KLF5, KLF6, BMP2, ESRRB, IL6, CEBPB, IRF8, IRF1, PRX1, MAFA, MAMLI1, SMDA3, CEBPB, NR4A2, ESRG, NR4A1, SMDA3, SMDA1, NR4A3, KLF15, TADA3, SREBF2, ATFA, SALLA, EAF1, CSRP1, KLF2, KLF4, PPARG, CHURCH1, FOXK1, ELFA, FOS, SDRP, YAP1, MYC, FGFR2, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGAI1, SMO, MURC, CANDI, FOXK1, INGS, ABLIM2, ABLIM3, GLI2, NUPP1, PRDM16, TNFRSF1A, REL, NFAT5, BCL3, MYOG, CEBPA, BCDHA, MYT6, IL6, CEBPB, CEBPD, TBK1, AFF1, STAT1, IRF8, IRF1, PRX1, RBM14, RBM15, NFIA, ARAP1	2080	358	13588	1.62	9.72E-03	2.64E-04	4.41E-03
GOTERM_BP_FAT	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	89	3.10	2.56E-06	MYOD1, THRB, TGFB3, TLR2, TLR4, PNP, TGFB1, CTGTD, KDM1A, MYO8B, TRNP3, RARA, RARB, BC10, RLA, SIZ2, ARNT1, SIK4, MED13, PPARGC1B, HXD09, HF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NEF2L2, FUS, HMG2R, CYYL1, SOX4, SP1, SOX9, PLAGL1, SLC11A1, TADA, AGRN, RUNX1, RUNX2, TRPS3, BMP4, KLF5, KLF6, ESRRB, BMP2, EPAS1, IZ2F1, MAFA, MAMLI1, SMDA3, CEBPB, NR4A2, ESRG, NR4A1, SMDA3, SMDA1, NR4A3, KLF15, TADA3, SREBF2, ATFA, SALLA, EAF1, CSRP1, KLF2, KLF4, PPARG, CHURCH1, FOXK1, ELFA, FOS, SDRP, YAP1, FGFR2, MYC, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGAI1, SMO, MURC, CANDI, FOXK1, INGS, ABLIM2, ABLIM3, GLI2, NUPP1, PRDM16, TNFRSF1A, REL, NFAT5, BCL3, MYOG, CEBPA, BCDHA, MYT6, IL6, CEBPB, CEBPD, TBK1, AFF1, STAT1, IRF8, IRF1, PRX1, RBM14, RBM15, NFIA, ARAP1	2080	475	13588	1.53	1.21E-02	2.98E-04	5.52E-03
GOTERM_BP_FAT	GO:0045943	positive regulation of transcription	111	3.87	2.96E-06	MYOD1, THRB, TGFB3, TLR2, TLR4, PNP, TGFB1, CTGTD, KDM1A, MYO8B, TRNP3, RARA, RARB, BC10, RLA, SIZ2, ARNT1, SIK4, MED13, PPARGC1B, HXD09, HXD09, HF1A, MED15, ZFP462, JUN, VEGFA, SIK1, MND4, VGLL2, TGFB1, FUS, HMG2R, CYYL1, SOX4, ABCA2, TNNI, SOX9, MEIS1, PLAGL1, SLC11A1, HEXIM1, TADA, AGRN, RUNX1, RUNX2, TRPS3, BMP4, KLF5, BMP2, ESRRB, EPAS1, IZ2F1, MAFA, MAMLI1, SMDA3, CEBPB, NR4A2, ESRG, NR4A1, SMDA3, SMDA1, NR4A3, KLF15, TADA3, SREBF2, ATFA, SALLA, EAF1, CSRP1, KLF2, KLF4, PPARG, CHURCH1, FOXK1, ELFA, FOS, SDRP, YAP1, MYC, FGFR2, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGAI1, SMO, MURC, CANDI, FOXK1, INGS, ABLIM2, ABLIM3, GLI2, NUPP1, PRDM16, TNFRSF1A, REL, NFAT5, BCL3, MYOG, CEBPA, BCDHA, MYT6, IL6, CEBPB, CEBPD, TBK1, AFF1, STAT1, IRF8, IRF1, PRX1, RBM14, RBM15, NFIA, ARAP1	2080	488	13588	1.51	1.54E-02	3.18E-04	7.02E-03
GOTERM_BP_FAT	GO:0010628	positive regulation of gene expression	113	3.94	3.72E-06	MYOD1, THRB, TGFB3, TLR2, TLR4, PNP, TGFB1, CTGTD, KDM1A, MYO8B, TRNP3, RARA, RARB, BC10, RLA, SIZ2, ARNT1, SIK4, MED13, PPARGC1B, HXD09, HXD09, HF1A, MED15, ZFP462, JUN, VEGFA, SIK1, MND4, VGLL2, TGFB1, FUS, HMG2R, CYYL1, SOX4, ABCA2, TNNI, SOX9, MEIS1, PLAGL1, SLC11A1, HEXIM1, TADA, AGRN, RUNX1, RUNX2, TRPS3, BMP4, KLF5, BMP2, ESRRB, EPAS1, IZ2F1, MAFA, MAMLI1, SMDA3, CEBPB, NR4A2, ESRG, NR4A1, SMDA3, SMDA1, NR4A3, KLF15, TADA3, SREBF2, ATFA, SALLA, EAF1, CSRP1, KLF2, KLF4, PPARG, CHURCH1, FOXK1, ELFA, FOS, SDRP, YAP1, MYC, FGFR2, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGAI1, SMO, MURC, CANDI, FOXK1, INGS, ABLIM2, ABLIM3, GLI2, NUPP1, PRDM16, TNFRSF1A, REL, NFAT5, BCL3, MYOG, CEBPA, BCDHA, MYT6, IL6, CEBPB, CEBPD, TBK1, AFF1, STAT1, IRF8, IRF1, PRX1, RBM14, RBM15, NFIA, ARAP1	2080	488	13588	1.51	1.54E-02	3.18E-04	7.02E-03
GOTERM_BP_FAT	GO:0006357	regulation of transcription from RNA polymerase II promoter	136	4.74	5.27E-06	MYOD1, THRB, TGFB3, TLR2, TLR4, PNP, TGFB1, CTGTD, KDM1A, MYO8B, TRNP3, RARA, RARB, BC10, RLA, SIZ2, ARNT1, SIK4, MED13, PPARGC1B, HXD09, HXD09, HF1A, MED15, ZFP462, JUN, VEGFA, SIK1, MND4, VGLL2, TGFB1, FUS, HMG2R, CYYL1, SOX4, ABCA2, TNNI, SOX9, MEIS1, PLAGL1, SLC11A1, HEXIM1, TADA, AGRN, RUNX1, RUNX2, TRPS3, BMP4, KLF5, BMP2, ESRRB, EPAS1, IZ2F1, MAFA, MAMLI1, SMDA3, CEBPB, NR4A2, ESRG, NR4A1, SMDA3, SMDA1, NR4A3, KLF15, TADA3, SREBF2, ATFA, SALLA, EAF1, CSRP1, KLF2, KLF4, PPARG, CHURCH1, FOXK1, ELFA, FOS, SDRP, YAP1, MYC, FGFR2, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGAI1, SMO, MURC, CANDI, FOXK1, INGS, ABLIM2, ABLIM3, GLI2, NUPP1, PRDM16, TNFRSF1A, REL, NFAT5, BCL3, MYOG, CEBPA, BCDHA, MYT6, IL6, CEBPB, CEBPD, TBK1, AFF1, STAT1, IRF8, IRF1, PRX1, RBM14, RBM15, NFIA, ARAP1	2080	616	13588	1.44	2.15E-02	4.10E-04	9.82E-03
GOTERM_BP_FAT	GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic proc	116	4.04	6.74E-06	MYOD1, THRB, TGFB3, PNP, TGFB1, CTGTD, KDM1A, MYO8B, TRNP3, RARA, RARB, BC10, RLA, SIZ2, ARNT1, SIK4, MED13, PPARGC1B, PTHLH, HXD09, HF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NEF2L2, FUS, HMG2R, ADORA2B, CYYL1, SOX4, SP1, SOX9, PLAGL1, SLC11A1, TADA, AGRN, RUNX1, RUNX2, TRPS3, BMP4, KLF5, KLF6, ESRRB, BMP2, EPAS1, IZ2F1, MAFA, MAMLI1, SMDA3, CEBPB, NR4A2, ESRG, NR4A1, SMDA3, SMDA1, NR4A3, KLF15, TADA3, SREBF2, ATFA, SALLA, EAF1, CSRP1, KLF2, KLF4, PPARG, CHURCH1, FOXK1, ELFA, FOS, SDRP, YAP1, MYC, FGFR2, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGAI1, SMO, MURC, CANDI, FOXK1, INGS, ABLIM2, ABLIM3, GLI2, NUPP1, PRDM16, TNFRSF1A, REL, NFAT5, BCL3, MYOG, CEBPA, BCDHA, MYT6, IL6, CEBPB, CEBPD, TBK1, AFF1, STAT1, IRF8, IRF1, PRX1, RBM14, RBM15, NFIA, ARAP1	2080	510	13588	1.49	2.74E-02	5.06E-04	1.26E-02
GOTERM_BP_FAT	GO:0010557	positive regulation of macromolecule biosynthetic process	119	4.15	9.65E-06	MYOD1, THRB, TGFB3, TLR2, TLR4, TGFB1, CTGTD, KDM1A, MYO8B, TRNP3, RARA, RARB, BC10, ICOSL2, RLA, SIZ2, ARNT1, SIK4, MED13, PPARGC1B, HXD09, HF1A, ZFP462, JUN, VEGFA, SIK1, VGLL2, NEF2L2, FUS, HMG2R, ADORA2B, CYYL1, SOX4, SP1, SOX9, PLAGL1, SLC11A1, TADA, AGRN, RUNX1, RUNX2, TRPS3, BMP4, KLF5, KLF6, ESRRB, BMP2, EPAS1, IZ2F1, MAFA, MAMLI1, SMDA3, CEBPB, NR4A2, ESRG, NR4A1, SMDA3, SMDA1, NR4A3, KLF15, TADA3, SREBF2, ATFA, SALLA, EAF1, CSRP1, KLF2, KLF4, PPARG, CHURCH1, FOXK1, ELFA, FOS, SDRP, YAP1, MYC, FGFR2, RHOG, SERTAD1, EGR1, AR, EGR2, TOPORS, HMGAI1, SMO, MURC, CANDI, FOXK1, INGS, ABLIM2, ABLIM3, GLI2, NUPP1, PRDM16, TNFRSF1A, REL, NFAT5, BCL3, MYOG, CEBPA, BCDHA, MYT6, IL6, CEBPB, CEBPD, TBK1, AFF1, STAT1, GSK, IRF8, IRF1, PRX1, RBM14, RBM15, NFIA, ARAP1	2080	530	13588	1.47	3.91E-02	6.87E-04	1.80E-03





GOTERM_MF_FAT	GO:0032555-purine ribonucleotide binding	356	12.46	4.82E-11	AMH2, ACTB, ALPK1, HKC, KIF18A, SMCC2, PCX, HSP90B1, ATPA2, APAF1, IPPK, H2-OMA, CDK20	1935	1796	13288	1.36	6.82E-08	1.70E-08	7.95E-08
GOTERM_MF_FAT	GO:0000166-nucleotide binding	413	14.46	7.12E-10	DHX34, DHX33, MAP2K6, RAB27A, PKC3G, GBP5, MYLK4, PFK1, MYLK2, MYH7, GEM, MYH9, MYH8, MAPK6, ARBA, MAPK7, GM1220, EF2AK3, ACADSB, GNA13, DN42, HSPA1A, ARF6, HSPA1B, NUSK, RAC2, PABPC1, DHX58, GPD1, FKH3, SPHK1, TAO3, UBE2L6, RAB7L1, VDAC1, KIF3C, VDAC2, VDAC1, ARF3, ARF4, PPKA1, HSP413, ACAD011, NUAK2, ATP10A, NOD2, SLC22A4, EF2K, SIK1, ARLSC, TARSL2, CD27, MAP2B, RAPA2, LYR, PHKG1, PDI10A, PDCD, 1700017805RK, MAST3, SGL, RPK1, EFPA1, ARK4D, ARAC, NASD1, ALDH18A1, USGN, PDI1A, MWN2, HK1, STK3A, FMO1, PTK28, HK1, CERK, PAP52, TRIP13, AC15, MYO3C, PDK2, ACT1, SWAP70, POK3, POK4, AXI, NADK, ACYL, RPS6A5, RPS6A4, RPS6K1, POLDIP3, ARAF, HPD0, GNA13, GNA15, RNASEL, HMGC, RMB1, RMB18B, RRAO, MTHFD1, DD27, PRAAR2B, RALB, DD21, STK39, SAR1B, RDM1, MATK, EGRF, NUDT2, FOXK, TWRF2, DOX39, ATP9A, OAS1A, LRK1, OAS16, SRN1, PPS2, GPD, FHN1, ASS1, STK10, MYTIC1A, TMPPA, CTP52, ABCA1, P2N6, MHNPP, HELLS, TEC, TRP53, ABCB9, RABBA, RABBA, MYO1C, MYO10, MYO1F, DD27, DOCK8, ABCB7, MMAB, IDH3A, DOX58, IKBKE, DN42, P2K4, PLK4, P2K7, DD256, P2K6, PLK3, PLK2, DYRK1B, POLD1, TUBD1, MERTK, IF22, ATL2, FDNL1, SFNPO, ATL3, SLFNK, CAD, FES, RHOF, SLFN4, SLFN1, SLFN2, RHOF, PDK3, CDK1, SGK1, ACAD0, KIF11, LMK1, CSK, MDN1, HK1, CD2, AK1, ATP9VIA, RNAS2, ERN1, TYNND1, DCK, ASN5, IGFB1, NAIIP2, TOR1A, HSPA5, EH01, DCLK1, EH04, AMH2, ALPK1, HKC, SMCC2, PCX, CYBB, HSP90B1, APAF1, IPPK, H2-OMA, ADCY7, AURKB, PRKX, SUTIA1, OAS2, OASL1, NTS2, GM4841, DOX10, RA820, BCK, IFAT, NAV3, WNK2, CARN1, RFC5, RND3, RFC1, ACAP1, PDGFR, RAB15, ARBA, RAB12, MAPK7, EF2AK3, SH3B4S22PK, CHA, PFKF81, PFKF81, OAS3, STX17B, CHEK1, MYO9B, IF2B2P2, OAS2, RAB408, TIC2, MYO10, ABCG2, ATP13A5, ABGCI, HSPA1, HYOU1, ATP2A2, GRK5, CLCN5, MYO7A, CAMKK1, CKB, CAMK2, ACTR3, ACTR2, MCC2, FANCM, TUBB8, TUBB6, RBA47, DOCK10, TOP2A, DOCK11, NTS2, TUBB3, DHCR24, NTS2, RAB4A, RAB4B, CBRA, GM1220, ADK, MAPK14, STEAP1, MYO5A, RAB3A, ITF, GCH1, GALK2, GALK1, RAB4A, RAB4B, MORC4, ABGCI, PPKA1A, MYO3C, NDS1, ATP1A1, ATP1A1, APRT, KHK, RAB2, GNA5A, RAB1, PYGM, PYGL, FYN, RAB3A, PHG01, ABCC3, GYK, RMB14, POK1, CTP5, F13A1, PH428, ITPKC, AR11, MLK1, MX1, MX2, RMB51, PNCK, CNGA3, STK4, POK, STK3, MAP4K4, PH42A, RPK3, PPS2, PCGA, GPN2, MXT1, ACTR1B, MAPK1, RRAO2, IRAKA, IRAK1, RHOTB2, EROL, UBE2D1, RNUK1, ENTPI1, CSF1R, RHOBTR3, EF1A1, AK1, EF1A2, ATAD2, PSMB8, PSMB9, RAB13B, ULK1, ULK2, NUSK, PHK2A, UBE2L1, CDK13, CDK17, DZHDH9, PPSK42, MKN7P, GSR, ACVRI1B, PAK2, PAK4, ATPB81, ATPB82,	1935	2183	13288	1.30	1.01E-06	1.68E-07	1.17E-06
GOTERM_MF_FAT	GO:0030554-adenyl nucleotide binding	295	10.33	9.02E-08	KRCC5, KIFC2, KIFC1, ADCY7, AURKC, C230081A13BK, PRKX, BTK, ERD18, DHX37, OAS12, OASL1, MAP3K8, DHX34, VPS48, DHX33, DOX10, MAP2K6, PKC3G, BCK, MYLK4, MYLK2, MYH7, WNK2, MYH9, MYH8, CARN1, RFC5, RFC3, MAPK6, ACAP1, PDGFR, MAPK7, EF2AK3, CHA, ACADSB, PFKF81, PFKF81, OAS3, STX17B, CHEK1, HSPA1A, MYO9B, HSPA1B, OAS2, TIC2, MYO10, MUSK, DHX58, IF3B, SPHK1, TAO3, UBE2L6, ABGCI, KIF3C, ATP13A5, EPNA2, ABGCI, HYOU1, ATP2A2, HSPA13, GRK5, ACAD011, CLCN5, NUAK2, MYO7A, ATP10A, CAMKK1, CAMK2, CKB, ACTR3, ACTR2, MCC2, FANCM, NOD2, SLC22A4, EF2K, SIK1, TOP2A, TABS2, DHCR24, CD27, LYR, PHKG1, PDCD, PDI10A, MAST3, SGL, ADK, RPK1, EFPA1, MAPK14, STEAP1, MYO5A, ALDH18A1, MKN2, HK1, KIT, GALK2, GALK1, MORC4, PTK28, HK1, ABGCI, PPKA1A, CERK, PAP52, TRIP13, AC15, MYO3C, PDK2, ACT1, SWAP70, POK3, POK4, ATP1A1, AXI, ACYL, NADK, ATP1A1, APRT, KHK, RPS6A5, RPS6A4, RPS6K1, FYN, ARAF, ABCB3, GYK, PGK1, RNASEL, CTP5, F13A1, ITPKC, PH428, MTHFD1, DD27, PRAAR2B, MLK1, STK39, DD21, MATE, EGRF, TWRF2, PDKX, PNCK, STK4, STK3, MAP4K4, DOX39, ATP9A, PH42A, RPK3, OAS1A, LRK1, OAS16, PCGA, EP40, SRN1, PPS2, GPD, FHN1, FOR, ASS1, ACTR3B, STK10, MAPK4, CTP52, TMPPA, ABCA1, IRAKA, IRAK1, EROL, UBE2D1, ENTPI1, RNUK1, HELLS, CSF1R, TEC, RHOBTR3, TRP53, ABCB9, MYO1C, AK1, MYO10, ATAD2, MYO1F, ABCB7, PSMB8, MMAB, PSMB9, DOX58, IKBKE, P2K4, DN42, P2K7, DOX56, PLK4, P2K6, PLK3, PLK2, ULYK1, DYRK1B, MERTK, PHK2A, UBE2L1, CDK13, CDK17, DZHDH9, PPSK42, MKN7P, GSR, ACVRI1B, PAK2, PAK4, ATPB81, ATPB82, MKK5, CSK, MDN1, CDK14, ATPB84, PRKCA, IRAK2, CDK1, SGK1, KIF11, HSP90A1, LMK1, PRKCI, CDK6, PFKM, PFK, UBE2H, MCMA3, NLRP3, PRKCD, MCMA, UBE2B, CDK2, MCMS, DAPK1, PRKCB, MCMA, PANKA, ATP9VIA, PRKCD, HSP9, ERN1, H2-AA, TYNND1, CAMK1D, UBE2Z, DCK, TUBB3, ASN5, TRB1, IGFB1, NAIIP2, TAP2, TAP1, TOR1A, PRKRYE, CAMK2B, UCK2, HSPA5, EH01, CAMK2A, DCLK1, EH04, AMH2, ACTB, ALPK1, HKC, KIF18A, SMCC2, PCX, HSP90B1, CYBB, ATPB82, APAF1, IPPK, H2-OMA, CDK20	1935	1535	13288	1.32	1.28E-04	1.59E-05	1.49E-04
GOTERM_MF_FAT	GO:00001887-purine nucleotide binding	296	10.36	1.32E-07	KRCC5, KIFC2, KIFC1, ADCY7, AURKC, C230081A13BK, PRKX, BTK, DHX37, OAS12, OASL1, MAP3K8, DHX34, VPS48, DHX33, DOX10, MAP2K6, PKC3G, BCK, MYLK4, MYLK2, MYH7, WNK2, MYH9, MYH8, CARN1, RFC5, RFC3, MAPK6, ACAP1, PDGFR, MAPK7, EF2AK3, CHA, ACADSB, PFKF81, PFKF81, OAS3, STX17B, CHEK1, HSPA1A, MYO9B, HSPA1B, OAS2, TIC2, MYO10, MUSK, DHX58, IF3B, SPHK1, TAO3, UBE2L6, ABGCI, KIF3C, ATP13A5, EPNA2, ABGCI, HYOU1, ATP2A2, HSPA13, GRK5, ACAD011, CLCN5, NUAK2, MYO7A, ATP10A, CAMKK1, CAMK2, CKB, ACTR3, MCC2, ACTR2, FANCM, NOD2, SLC22A4, EF2K, SIK1, TOP2A, TABS2, DHCR24, CD27, LYR, PHKG1, PDCD, PDI10A, MAST3, SGL, ADK, RPK1, EFPA1, MAPK14, STEAP1, MYO5A, ALDH18A1, MKN2, HK1, KIT, GALK2, GALK1, MORC4, PTK28, HK1, ABGCI, PPKA1A, CERK, PAP52, TRIP13, AC15, MYO3C, PDK2, ACT1, SWAP70, POK3, POK4, ATP1A1, AXI, ACYL, NADK, ATP1A1, APRT, KHK, RPS6A5, RPS6A4, RPS6K1, FYN, ARAF, ABCB3, GYK, PGK1, RNASEL, CTP5, F13A1, ITPKC, PH428, MTHFD1, DD27, PRAAR2B, MLK1, STK39, DD21, MATE, EGRF, TWRF2, PDKX, PNCK, CNGA3, STK4, STK3, MAP4K4, DOX39, ATP9A, PH42A, RPK3, OAS1A, LRK1, OAS16, PCGA, EP40, SRN1, PPS2, GPD, FHN1, FOR, ASS1, ACTR3B, STK10, MAPK4, CTP52, TMPPA, ABCA1, IRAKA, IRAK1, EROL, UBE2D1, ENTPI1, RNUK1, HELLS, CSF1R, TEC, RHOBTR3, TRP53, ABCB9, MYO1C, AK1, MYO10, ATAD2, MYO1F, ABCB7, PSMB8, MMAB, PSMB9, DOX58, IKBKE, P2K4, DN42, P2K7, DOX56, PLK4, P2K6, PLK3, PLK2, ULYK1, DYRK1B, MERTK, PHK2A, UBE2L1, CDK13, CDK17, DZHDH9, PPSK42, MKN7P, GSR, ACVRI1B, PAK2, PAK4, ATPB81, ATPB82, MKK5, CSK, MDN1, CDK14, ATPB84, PRKCA, IRAK2, CDK1, SGK1, KIF11, HSP90A1, LMK1, PRKCI, CDK6, PFKM, PFK, UBE2H, MCMA3, NLRP3, PRKCD, MCMA, UBE2B, CDK2, MCMS, DAPK1, PRKCB, MCMA, PANKA, ATP9VIA, PRKCD, HSP9, ERN1, H2-AA, TYNND1, CAMK1D, UBE2Z, DCK, TUBB3, ASN5, TRB1, IGFB1, NAIIP2, TAP2, TAP1, TOR1A, PRKRYE, CAMK2B, UCK2, HSPA5, EH01, CAMK2A, DCLK1, EH04, AMH2, ACTB, ALPK1, HKC, KIF18A, SMCC2, PCX, HSP90B1, CYBB, ATPB82, APAF1, IPPK, H2-OMA, CDK20	1935	1548	13288	1.31	1.87E-04	1.70E-05	2.17E-04
GOTERM_MF_FAT	GO:0032559-adenyl ribonucleotide binding	281	9.84	1.66E-07	KRCC5, KIFC2, KIFC1, ADCY7, AURKC, C230081A13BK, PRKX, BTK, DHX37, OAS12, OASL1, MAP3K8, DHX34, VPS48, DHX33, DOX10, MAP2K6, PKC3G, BCK, MYLK4, MYLK2, MYH7, WNK2, MYH9, MYH8, CARN1, RFC5, RFC3, MAPK6, ACAP1, PDGFR, MAPK7, EF2AK3, CHA, ACADSB, PFKF81, PFKF81, OAS3, STX17B, CHEK1, HSPA1A, MYO9B, HSPA1B, OAS2, TIC2, MYO10, MUSK, DHX58, IF3B, SPHK1, TAO3, UBE2L6, ABGCI, KIF3C, ATP13A5, EPNA2, ABGCI, HYOU1, ATP2A2, HSPA13, GRK5, CLCN5, NUAK2, MYO7A, ATP10A, CAMKK1, CAMK2, CKB, ACTR3, MCC2, ACTR2, FANCM, NOD2, SLC22A4, EF2K, SIK1, TOP2A, TABS2, DHCR24, CD27, LYR, PHKG1, PDCD, PDI10A, MAST3, ADK, RPK1, EFPA1, MAPK14, STEAP1, MYO5A, ALDH18A1, MKN2, HK1, KIT, GALK2, GALK1, MORC4, PTK28, HK1, ABGCI, PPKA1A, CERK, PAP52, TRIP13, AC15, MYO3C, PDK2, ACT1, SWAP70, POK3, POK4, ATP1A1, AXI, ACYL, NADK, ATP1A1, APRT, KHK, RPS6A5, RPS6A4, RPS6K1, FYN, ARAF, ABCB3, GYK, PGK1, RNASEL, CTP5, F13A1, ITPKC, PH428, MTHFD1, DD27, PRAAR2B, MLK1, STK39, DD21, MATE, EGRF, TWRF2, PDKX, PNCK, CNGA3, STK4, STK3, MAP4K4, DOX39, ATP9A, PH42A, RPK3, OAS1A, LRK1, OAS16, PCGA, EP40, SRN1, PPS2, GPD, FHN1, FOR, ASS1, ACTR3B, STK10, MAPK4, CTP52, TMPPA, ABCA1, IRAKA, IRAK1, EROL, UBE2D1, ENTPI1, RNUK1, HELLS, CSF1R, TEC, RHOBTR3, TRP53, ABCB9, MYO1C, AK1, MYO10, ATAD2, MYO1F, ABCB7, PSMB8, MMAB, PSMB9, DOX58, IKBKE, P2K4, DN42, P2K7, DOX56, PLK4, P2K6, PLK3, PLK2, ULYK1, DYRK1B, MERTK, PHK2A, UBE2L1, CDK13, CDK17, DZHDH9, PPSK42, MKN7P, GSR, ACVRI1B, PAK2, PAK4, ATPB81, ATPB82, MKK5, CSK, MDN1, CDK14, ATPB84, PRKCA, IRAK2, CDK1, SGK1, KIF11, HSP90A1, LMK1, PRKCI, CDK6, PFKM, PFK, UBE2H, MCMA3, NLRP3, PRKCD, MCMA, UBE2B, CDK2, MCMS, DAPK1, PRKCB, MCMA, PANKA, ATP9VIA, PRKCD, HSP9, ERN1, H2-AA, TYNND1, CAMK1D, UBE2Z, DCK, TUBB3, ASN5, TRB1, IGFB1, NAIIP2, TAP2, TAP1, TOR1A, PRKRYE, CAMK2B, UCK2, HSPA5, EH01, CAMK2A, DCLK1, EH04, AMH2, ACTB, ALPK1, HKC, KIF18A, SMCC2, PCX, HSP90B1, CYBB, ATPB82, APAF1, IPPK, H2-OMA, CDK20	1935	1460	13288	1.32	2.35E-04	1.96E-05	2.74E-04

[illegible]

GOTERM_BP_FAT	GO:0001819-positive regulation of cytokine production	25	0.88	6.33E-06	PANK1, ADD3A2B, TIR2, TIR4, TIR7, SLIC11A, NOD2, MYD88, TICAM1, PYCARD, FCGR1B, IL18, RCL3, CASP1, CARD8, H2-M3, CD40, NLRP3, IFNAR1, DDX58, CD28, P2RX7, CLEC7A, SASH3, CD14	2019	62	13588	2.71	1.44E-02	2.79E-04	6.74E-03
Annotation Cluster 10 Category	Enrichment Score: 5.378544778286805 Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0408002-antigen processing and presentation of peptide antigen	21	0.74	8.51E-09	FCGR1B, B2M, SLIC11A, FCGR2B, H2-DME1, H2-EB1, FCER1G, H2-A4, H2-T2, IL2, DMA	2019	35	13588	4.04	3.41E-05	1.89E-06	1.58E-05
GOTERM_BP_FAT	GO:0002478-antigen processing and presentation of exogenous peptide antigen	16	0.56	5.39E-08	H2-M3, UNC93B1, 2610524H06R1K, IF30, H2-DME1, H2-A81, FCGR1, CD74, B2M, FCGR3, FCGR2B, TAP2, H2-EB1, FCER1G, H2-AA, H2-DMA	2019	23	13588	4.68	2.16E-04	9.38E-06	1.00E-04
GOTERM_BP_FAT	GO:0019884-antigen processing and presentation of exogenous antigen	16	0.56	1.96E-06	H2-M3, UNC93B1, 2610524H06R1K, IF30, H2-DME1, H2-A81, FCGR1, CD74, B2M, FCGR3, FCGR2B, TAP2, H2-EB1, FCER1G, H2-AA, H2-DMA	2019	28	13588	3.85	7.83E-03	1.60E-04	3.65E-03
GOTERM_BP_FAT	GO:0019885-antigen processing and presentation of peptide peptide antigen via MHC class II	11	0.39	1.73E-05	FCGR2B, H2-EB1, UNC93B1, 2610524H06R1K, H2-AA, FCER1G, H2-DME1, IF30, H2-A81, H2-DMA, CD74	2019	16	13588	4.65	6.69E-02	1.02E-03	3.21E-02
GOTERM_BP_FAT	GO:0002495-antigen processing and presentation of peptide antigen via MHC class II	11	0.39	1.73E-05	FCGR2B, H2-EB1, UNC93B1, 2610524H06R1K, H2-AA, FCER1G, H2-DME1, IF30, H2-A81, H2-DMA, CD74	2019	16	13588	4.63	6.69E-02	1.02E-03	3.21E-02
Annotation Cluster 11 Category	Enrichment Score: 5.143700989844686 Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0012501-programmed cell death	107	3.75	5.42E-06	ADAM1, PMAIP1, TGFBR1, CRADD, CLPTM1L, SHB, APP, CUL7, NGFRAP1, DAP, CIB1, SGPL1, BCL10, NCF1, MADD, FADD, TNFRSF14, STK4, BCL2L11, STK3, TRIM35, KRT18, TNFAIP8, RIPK3, PDCD6IP, MARK7, TNFAIP3, IF2AK3, TRAF1, LST1, LITAF, TNFRSF12A, CLU, STK17B, ARF6, PTT1, BCL2L1, SP110, IRAK3, PRUNE2, GJ2, FAIM, SRGN, TRP53, CDAP2, RYBP, VDAC1, CDC6, TRADD, TRADD, BBCL3, CSNRP1, E2F3, NUA2, BNIP3, CKC2, CASP6, TMEM173, CASP3, CASP4, PAK2, CASP9, CASP8, TICAM1, CASP1, MYC, LTB, IRAK2, SGK1, CYCS, NLRP3, DNASE2A, DAPK1, ELMO1, TNFRSF10B, RIPK1, GADD45G, SH3KBP1, ERN1, MFSO10, NGFR, PPP1R15A, BID, UBE2Z, PML, TRB3, KIT, FEM1B, TNFRSF14, TNFRSF1B, NARP2, RCL2, NARPS, SHSAS, KRT6, PCDAR, ZCCH12A, INPP5D, XAF1, PHDLA1, ACTC1, IL6, AIMP2, EDAR3, PEAS1A, PPP1R13L, RASFS5, BAX, ENDOG, APAF1, APP, DRAM1	2019	473	13588	1.52	2.15E-02	3.87E-04	1.01E-02
GOTERM_BP_FAT	GO:0008219-cell death	113	3.96	5.90E-06	ADAM1, PMAIP1, TGFBR1, CRADD, CLPTM1L, SHB, APP, CUL7, NGFRAP1, DAP, CIB1, SGPL1, BCL10, NCF1, MADD, FADD, TNFRSF14, STK4, BCL2L11, STK3, TRIM35, KRT18, TNFAIP8, RIPK3, PDCD6IP, MARK7, TNFAIP3, IF2AK3, TRAF1, LST1, LITAF, TNFRSF12A, CLU, STK17B, ARF6, PTT1, BCL2L1, SP110, IRAK3, PRUNE2, GJ2, FAIM, SRGN, TRP53, CDAP2, RYBP, VDAC1, CDC6, TRADD, TRADD, BBCL3, CSNRP1, E2F3, NUA2, BNIP3, CKC2, CASP6, TMEM173, CASP3, CASP4, PAK2, CASP9, CASP8, TICAM1, CASP1, MYC, LTB, IRAK2, SGK1, CYCS, NLRP3, DNASE2A, DAPK1, ELMO1, TNFRSF10B, RIPK1, GADD45G, SH3KBP1, ERN1, MFSO10, NGFR, PPP1R15A, BID, UBE2Z, PML, TRB3, KIT, FEM1B, TNFRSF14, TNFRSF1B, NARP2, RCL2, NARPS, SHSAS, KRT6, PCDAR, ZCCH12A, INPP5D, XAF1, PHDLA1, ACTC1, IL6, AIMP2, PEAS1A, PPP1R13L, RASFS5, BAX, ENDOG, APAF1, APP, DRAM1	2019	507	13588	1.50	2.33E-02	4.14E-04	1.10E-02
GOTERM_BP_FAT	GO:0006915-apoptosis	105	3.68	7.21E-06	ADAM1, PMAIP1, CRADD, SHB, CLPTM1L, APP, CUL7, NGFRAP1, DAP, CIB1, SGPL1, BCL10, MADD, NCF1, FADD, TNFRSF14, STK4, BCL2L11, STK3, TRIM35, KRT18, TNFAIP8, RIPK3, PDCD6IP, MARK7, TNFAIP3, IF2AK3, TRAF1, LST1, LITAF, TNFRSF12A, CLU, STK17B, ARF6, PTT1, BCL2L1, SP110, IRAK3, PRUNE2, GJ2, FAIM, SRGN, TRP53, CDAP2, RYBP, VDAC1, CDC6, TRADD, TRADD, BBCL3, CSNRP1, E2F3, NUA2, BNIP3, CKC2, CASP6, TMEM173, CASP3, CASP4, PAK2, CASP9, CASP8, TICAM1, CASP1, MYC, LTB, IRAK2, SGK1, CYCS, NLRP3, DNASE2A, DAPK1, ELMO1, TNFRSF10B, RIPK1, GADD45G, SH3KBP1, ERN1, MFSO10, NGFR, PPP1R15A, BID, UBE2Z, PML, TRB3, KIT, FEM1B, TNFRSF14, TNFRSF1B, NARP2, RCL2, NARPS, SHSAS, KRT6, PCDAR, ZCCH12A, INPP5D, XAF1, PHDLA1, ACTC1, IL6, AIMP2, PEAS1A, PPP1R13L, RASFS5, BAX, ENDOG, APAF1, APP, DRAM1	2019	465	13588	1.52	2.85E-02	4.81E-04	1.34E-02
GOTERM_BP_FAT	GO:0016265-death	114	3.99	1.09E-05	ADAM1, PMAIP1, TGFBR1, CRADD, CLPTM1L, SHB, APP, CUL7, NGFRAP1, DAP, CIB1, SGPL1, BCL10, NCF1, MADD, FADD, TNFRSF14, STK4, BCL2L11, STK3, TRIM35, KRT18, TNFAIP8, RIPK3, PDCD6IP, MARK7, TNFAIP3, IF2AK3, TRAF1, LST1, LITAF, TNFRSF12A, CLU, STK17B, ARF6, PTT1, BCL2L1, SP110, IRAK3, PRUNE2, GJ2, FAIM, SRGN, TRP53, CDAP2, RYBP, VDAC1, CDC6, TRADD, TRADD, BBCL3, CSNRP1, E2F3, NUA2, BNIP3, CKC2, CASP6, TMEM173, CASP3, CASP4, PAK2, CASP9, CASP8, TICAM1, CASP1, MYC, LTB, IRAK2, SGK1, CYCS, NLRP3, DNASE2A, DAPK1, ELMO1, TNFRSF10B, RIPK1, GADD45G, SH3KBP1, ERN1, MFSO10, NGFR, PPP1R15A, BID, UBE2Z, PML, TRB3, KIT, FEM1B, TNFRSF14, TNFRSF1B, NARP2, RCL2, NARPS, SHSAS, KRT6, PCDAR, ZCCH12A, INPP5D, XAF1, PHDLA1, ACTC1, IL6, AIMP2, PEAS1A, PPP1R13L, RASFS5, BAX, ENDOG, APAF1, APP, DRAM1	2019	519	13588	1.48	4.28E-02	6.84E-04	2.03E-02
Annotation Cluster 12 Category	Enrichment Score: 4.768117672113028 Term	Count %										

[illegible]

GOTERM_MF_FAT	GO:0005096~GTPase activator activity	IQGAP2, ARHGAP15, TBC1D19, IQGAP1, TBC1D16, HMHA1, ARHGAP22, ARHGAP20, RIN1, TIAM2, ARHGAP1, RANBP1, ARHGAP11A, ARHGAP9, ROR, ARHGAP28, SIPA1L1, THY1, ARHGAP25, ARHGAP30, ACAP1, RIN1, RIN3, ARFGAP2, ARHGDI6, ARFGAP3, RAP1GAP, TBC1D9, GPM3, SIPA1, MYO9B, FAM138, ADAP1, DOCK2, RGS12, GMIP, GPM1, RASA3, ARHGDA, ARHGDI8, TBC1D2, TBC1D28, TBC1D10C, ABR, TBC1D10A, RGS18, RGS16, RACGAP1, RGS14, USPEN1, ADAP2, RGS2, CHML, GRTF1, SH3BP1, ARAP1									
		56	1.96	3.05E-07	1935	192	13288	2.00	4.32E-04	2.70E-05	5.03E-04

Table SLD GO Terms upregulated 48 hours post injury

Category	Term	Count	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030029-actin filament-based process	54	2.51	3.73E-11	TLN1, LIMA1, AIF1, S100A9, CAPZA1, RHOG, ACTG1, RHOA, CAP1, RHOG, FMNL1, DBNL, ARHGEF2, ACTN4, ACTN1, TMSB10, MYH9, SRPA, WAS, VASP, FLNA, ELMO1, FMNL, XIRP1, CFL1, TMSB4X, LCP1, MYO5A, MYH5, SHROOM3, TCAP, MYL2, ARPC4, CALR, FNZ, E2F, RAC2, SH2B2, CNN2, INF2, CSRP1, RACGAP1, GAS7, CAPN3, EPB4.1L2, CORO1C, NMAS, CORO1A, EPB4.1L1, EPB8, EPB4.1, TMOD1	1594	176	13588	2.62	1.36E-07	2.26E-08	6.87E-08
					TLN1, LIMA1, AIF1, S100A9, CAPZA1, RHOG, ACTG1, RHOA, CAP1, RHOG, FMNL1, DBNL, ARHGEF2, ACTN4, ACTN1, TMSB10, MYH9, SRPA, WAS, VASP, FLNA, ELMO1, FMNL, XIRP1, CFL1, TMSB4X, LCP1, SHROOM3, TCAP, MYL2, ARPC4, CALR, FNZ, E2F, RAC2, SH2B2, CNN2, INF2, CSRP1, RACGAP1, GAS7, CAPN3, EPB4.1L2, CORO1C, NMAS, CORO1A, EPB4.1L1, EPB8, EPB4.1, TMOD1	1594	165	13588	2.58	1.27E-06	1.06E-07	6.42E-07
GOTERM_BP_FAT	GO:0030036-actin cytoskeleton organization	50	2.32	3.49E-10	TLN1, LIMA1, AIF1, CAPZA1, S100A9, RHOG, VIL1, ACTG1, TUBB8, RHOA, RANBP1, CAP1, TUBA18, RHOG, FMNL1, DBNL, ARHGEF2, KIF11, ACTN4, ACTN1, NUSAP1, TMSB10, ESP1, PIK1S1, MYH9, TACC3, WAS, SRPA, UBE2B, FLNA, VASP, THY1, ELMO1, FMNL, SGC6, XIRP1, TPPP, CFL1, TMSB4X, TMNL1, GAD65A, LCP1, SHROOM3, MYH2, TCAP, ARPC4, CALX, FMR1, G2E, RAC2, SH2B2, CNN2, E2F, RAC2, FMOX2, CMN2, SH2B2, TES, SYNPO, INF2, CEF192, BRCC5, CSRP1, RACGAP1, GAS7, CAPN3, BRCA1, CORO1C, EPB4.1L2, NRAS, CORO1A, VYHAAH, EPB4.1L1, EPB8, LASP1, SVIL, EPB4.1, TMOD1	1594	326	13588	1.99	1.82E-05	1.40E-06	9.21E-06
					TLN1, LIMA1, AIF1, CAPZA1, S100A9, RHOG, VIL1, ACTG1, TUBB8, RHOA, RANBP1, CAP1, TUBA18, RHOG, FMNL1, DBNL, ARHGEF2, KIF11, ACTN4, ACTN1, NUSAP1, TMSB10, ESP1, PIK1S1, MYH9, TACC3, WAS, SRPA, UBE2B, FLNA, VASP, THY1, ELMO1, FMNL, SGC6, XIRP1, TPPP, CFL1, TMSB4X, TMNL1, GAD65A, LCP1, SHROOM3, MYH2, TCAP, ARPC4, CALX, FMR1, G2E, RAC2, SH2B2, CNN2, E2F, RAC2, FMOX2, CMN2, SH2B2, TES, SYNPO, INF2, CEF192, BRCC5, CSRP1, RACGAP1, GAS7, CAPN3, BRCA1, CORO1C, EPB4.1L2, NRAS, CORO1A, VYHAAH, EPB4.1L1, EPB8, LASP1, SVIL, EPB4.1, TMOD1	1594	326	13588	1.99	1.82E-05	1.40E-06	9.21E-06
Annotation Cluster 2	Enrichment Score: 8.96343293736693	Count <th>%</th> <th>Pvalue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
	Term				PRKAG3, PPARG, LDHB, GNPDA1, PHK8, PGD, PGAM1, PGAM2, OGDH, HIBADH, PPP1R1A, PDHA1, MAN2B1, MYC, ALDH5A1, PHKG1, FBP2, PPP1R3A, PGML2, PGML2, MAN2A2, MAN2A1, RENBP, PGML1, MDH1, PFKFB3, PFKFB1, SLC7A4, PHA1, HK1, GALK2, PPP1R3B, INO2, GYS1, GALE, AGL, ENO1, GPD2, PKD2, GPD1, WOTC1, GMSD, FOK3, EPB2A, BFGM, DIAT, MAN1C1, CTPIA, AT3, PYGL, FABP5, PYGB	1594	169	13588	2.62	2.92E-07	3.24E-08	1.47E-07
GOTERM_BP_FAT	GO:0019318-hexose metabolic process	52	2.42	8.01E-11	PRKAG3, PPARG, LDHB, GNPDA1, PHK8, PGD, PGAM1, PGAM2, OGDH, HIBADH, PPP1R1A, PDHA1, MAN2B1, MYC, ALDH5A1, PHKG1, FBP2, PPP1R3A, PGML2, PGML2, MAN2A2, MAN2A1, RENBP, PGML1, MDH1, PFKFB3, PFKFB1, SLC7A4, PHA1, HK1, GALK2, PPP1R3B, INO2, GYS1, GALE, AGL, ENO1, GPD2, PKD2, GPD1, WOTC1, GMSD, FOK3, EPB2A, BFGM, DIAT, MAN1C1, CTPIA, AT3, PYGL, FABP5, PYGB	1594	191	13588	2.45	1.23E-06	1.12E-07	6.24E-07
					PRKAG3, LDHB, PPARG, PHB8, PHA1, SLC7A4, PGD, PGAM1, PGAM2, HK1, OGDH, HIBADH, PPP1R3B, PPP1R3A, INO2, GYS1, PDHA1, MYC, AGL, ENO1, GPD2, GPD1, WOTC1, PHKG1, ALDH5A1, RENBP, PGML1, EPB2A, BFGM, DIAT, FBP2, PPP1R3A, CTPIA, PGML2, PGAM2, AT3, PYGL, PGML1, FABP5, MDH1, CSGLNACT1, AT3, PYGL, FABP5, PYGB	1594	191	13588	2.45	1.23E-06	1.12E-07	6.24E-07
GOTERM_BP_FAT	GO:0005996-monosaccharide metabolic process	55	2.56	3.39E-10	PRKAG3, LDHB, PPARG, PHB8, PHA1, SLC7A4, PGD, PGAM1, PGAM2, HK1, OGDH, HIBADH, PPP1R3B, PPP1R3A, INO2, GYS1, PDHA1, MYC, AGL, ENO1, GPD2, GPD1, WOTC1, PHKG1, ALDH5A1, RENBP, PGML1, EPB2A, BFGM, DIAT, FBP2, PPP1R3A, CTPIA, PGML2, PGAM2, AT3, PYGL, PGML1, FABP5, MDH1, CSGLNACT1, AT3, PYGL, FABP5, PYGB	1594	191	13588	2.45	1.23E-06	1.12E-07	6.24E-07
					PRKAG3, LDHB, PPARG, PHB8, PHA1, SLC7A4, PGD, PGAM1, PGAM2, HK1, OGDH, HIBADH, PPP1R3B, PPP1R3A, INO2, GYS1, PDHA1, MYC, AGL, ENO1, GPD2, GPD1, WOTC1, PHKG1, ALDH5A1, RENBP, PGML1, EPB2A, BFGM, DIAT, FBP2, PPP1R3A, CTPIA, PGML2, PGAM2, AT3, PYGL, PGML1, FABP5, MDH1, CSGLNACT1, AT3, PYGL, FABP5, PYGB	1594	191	13588	2.45	1.23E-06	1.12E-07	6.24E-07
GOTERM_BP_FAT	GO:0006006-glucose metabolic process	41	1.91	4.74E-08	PRKAG3, LDHB, PPARG, PHB8, PHA1, SLC7A4, PGD, PGAM1, PGAM2, HK1, OGDH, HIBADH, PPP1R3B, PPP1R3A, INO2, GYS1, PDHA1, MYC, AGL, ENO1, GPD2, GPD1, WOTC1, PHKG1, ALDH5A1, RENBP, PGML1, EPB2A, BFGM, DIAT, FBP2, PPP1R3A, CTPIA, PGML2, PGAM2, AT3, PYGL, PGML1, FABP5, MDH1, CSGLNACT1, AT3, PYGL, FABP5, PYGB	1594	140	13588	2.50	1.72E-04	7.84E-06	8.72E-05
	Annotation Cluster 3	Enrichment Score: 8.5768089676648	Count <th>%</th> <th>Pvalue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini
GOTERM_BP_FAT	GO:0009611-response to wounding	85	3.95	3.90E-11	GNA13, PPARG, LY86, F13A1, HPS1, TLR2, TLR4, TLR7, C1QC, TGFBI, TLR8, CFP, GPX1, CASP3, MYO8B, CD44, IL18, CITA, NFIB2, GATM, NCF1, LY96, MYH2, CD148, RAUJ, CAP, C1QB, SERPINA1, UNC119, HIF1A, THBD, CCR5, CCR2, CCR4, PPAR, IL1F1, PPAR, CCL2, CCL4, CXCL3, CXCL8, ITGB2, SPH10, CCL4, CCL7, CCL11, SLC11A1, TNFRSF1A, TNFRSF1B, TNFRSF18, MTPN, PICALM, ENTPD1, THBS1, FN1, PTPN6, KLFG, LIPA, PLEK, CFB, EFEMP2, SPHK1, TLR13, EPHK2, CHS13, ANKX5, FCGRI1, STAB1, CD180, FCGR2, SD02, HDAC5, NOTCH2, HT2L, SLC7A2, CXCL13, BAX, I33, ALOX5, CLEC7A, CD14, DRM2, KIF89A	1594	347	13588	2.09	1.42E-07	2.03E-08	7.18E-08
					LY86, TLR2, H2-D1, BNP3, TLR4, TLR6, TLR7, C1QC, TGFBI, TLR8, B2M, CFP, TMEM173, MYO8B, CD44, IL18AP, IL18, MX1, CITA, NFIB2, GATM, NCF1, LY96, MYH2, CD148, RAUJ, CAP, C1QB, C1QB, SERPINA1, UNC119, HIF1A, CCR5, CCR2, CCR4, PPAR, IL1F1, PPAR, CCL2, CCL4, CXCL3, CXCL8, ITGB2, SPH10, CCL4, CCL7, CCL11, SLC11A1, TNFRSF1A, TNFRSF1B, TNFRSF18, MTPN, PICALM, ENTPD1, THBS1, FN1, PTPN6, KLFG, LIPA, PLEK, CFB, EFEMP2, SPHK1, TLR13, EPHK2, CHS13, ANKX5, FCGRI1, STAB1, CD180, FCGR2, SD02, HDAC5, NOTCH2, HT2L, SLC7A2, CXCL13, BAX, I33, ALOX5, CLEC7A, CD14, DRM2, KIF89A	1594	347	13588	2.09	1.42E-07	2.03E-08	7.18E-08
GOTERM_BP_FAT	GO:0006952-defense response	94	4.37	1.86E-08	ARPC3, FCGR2B, STAB1, CD180, FCGR2, SD02, HDAC5, NOTCH2, HT2L, SLC7A2, CXCL13, BAX, I33, ALOX5, CLEC7A, CD14, DRM2, KIF89A, LY86, TLR2, TLR4, TLR6, TLR7, C1QC, TGFBI, TLR8, CFP, GPX1, CASP3, MYO8B, CD44, IL18, CITA, NFIB2, GATM, NCF1, LY96, MYH2, CD148, RAUJ, CAP, C1QB, SERPINA1, UNC119, HIF1A, THBD, CCR5, CCR2, CCR4, PPAR, IL1F1, PPAR, CCL2, CCL4, CXCL3, CXCL8, ITGB2, SPH10, CCL4, CCL7, CCL11, SLC11A1, TNFRSF1A, TNFRSF1B, TNFRSF18, MTPN, PICALM, ENTPD1, THBS1, FN1, PTPN6, KLFG, LIPA, PLEK, CFB, EFEMP2, SPHK1, TLR13, EPHK2, CHS13, ANKX5, FCGRI1, STAB1, CD180, FCGR2, SD02, HDAC5, NOTCH2, HT2L, SLC7A2, CXCL13, BAX, I33, ALOX5, CLEC7A, CD14, DRM2, KIF89A, OSM2	1594	448	13588	1.79	6.76E-05	3.76E-06	3.42E-05
					ARPC3, FCGR2B, STAB1, CD180, FCGR2, SD02, HDAC5, NOTCH2, HT2L, SLC7A2, CXCL13, BAX, I33, ALOX5, CLEC7A, CD14, DRM2, KIF89A, LY86, TLR2, TLR4, TLR6, TLR7, C1QC, TGFBI, TLR8, CFP, GPX1, CASP3, MYO8B, CD44, IL18, CITA, NFIB2, GATM, NCF1, LY96, MYH2, CD148, RAUJ, CAP, C1QB, SERPINA1, UNC119, HIF1A, THBD, CCR5, CCR2, CCR4, PPAR, IL1F1, PPAR, CCL2, CCL4, CXCL3, CXCL8, ITGB2, SPH10, CCL4, CCL7, CCL11, SLC11A1, TNFRSF1A, TNFRSF1B, TNFRSF18, MTPN, PICALM, ENTPD1, THBS1, FN1, PTPN6, KLFG, LIPA, PLEK, CFB, EFEMP2, SPHK1, TLR13, EPHK2, CHS13, ANKX5, FCGRI1, STAB1, CD180, FCGR2, SD02, HDAC5, NOTCH2, HT2L, SLC7A2, CXCL13, BAX, I33, ALOX5, CLEC7A, CD14, DRM2, KIF89A, OSM2	1594	225	13588	2.16	9.34E-05	4.67E-06	4.72E-05
GOTERM_BP_FAT	GO:0006954-inflammatory response	57	2.65	2.57E-08	KIF89A, OSM2	1594	225	13588	2.16	9.34E-05	4.67E-06	4.72E-05
					KIF89A, OSM2	1594	225	13588	2.16	9.34E-05	4.67E-06	4.72E-05
Annotation Cluster 4	Enrichment Score: 6.230189097120934	Count <th>%</th> <th>Pvalue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Bonferroni</th> <th>Benjamini</th> <th>FDR</th>	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
	Term				KIFC1, ADCY7, TUBB2B, TUBB2A, LDHG, PRKX, BTK, ACTG1, RAB28, OASL2, OASL1, MAP3K8, PRK3G, SUCLG1, MYH2, MYLK2, WNK2, GEM, MYH5, MYH8, RFC5, RND3, MAPK6, NME1, DID, PDGFRA, RAB12, MAPK7, S4304S522R1K, ACADSB, GNAI3, GNAI2, NEK2, PFKFB3, PFKFB1, STK17B, CHEK1, ARF6, MYO9B, OAS2, NAGK, HADHA, HSPA1L, MUSK, RAC2, IQH2, PAPBFL, BDNF, GCDH, GPD1, KIF8B, SPHK1, ARCG3, ATP13A1, VDAC1, ARCG1, VDAC1, ATP13A4, HYOU1, ATP2A2, ARF3, ARF4, TNF2, HSPA1A, ACAD11, CLCNK, SLC7A1, SPOT, BCKDK, RAB5C, KCN1J1, CAMK2K, CKB, ACTR3, MCC2, MCC1, TUBB8, TUBB6, MASTL, DOCK10, SIK1, TOP2A, DOCK11, TARSL2, NTSC2, CDC7, RAP2B, CDC6, RAP2A, LYN, PHKG1, RAB48, NDUFA13, PDCCC, 1700017808R1K, GMPHR, NDUFA10, MAST1, DNAC27, GM12250, SQLE, ADR, RIFP1, EF4A1, MAP3K10, RAB39, STEAP2, ARL4C, MYO5A, ALDH5A1, UGDH, POA1, HK1, GALK2, RAB4A, RAB43, PTK2B, ABCD2, BUB1, CERK, PRKAA2, KIF21B, ETFA, ACUL5, MYO5C, PKD2, NOS1, FDK3, ACV1, NADK, NRP2, ATP1A1, APRT, SDHA, RPS6KA5, RAB22, NRAS, ABCC9, RAB31, MAPK12, ADCY9, PYGL, RAB3A, HSPA4L, KIF20B, PHGDH, ARCC3, CHTF18, GYK, AACS, GNA13, RNASEL, DSERT0579E, HMGCR, RBBM5, F13A1, RABD, RAB28, MYTHD1L, PPKAR2B, ACS1, IDH3G, ORLH, GBP10, RABL, MUK1, SARIE, MX1, NSR, MYAT, CITA, MAP4K4, RIFP2, OAS1A, PCB, PCB, SHN1, FGR, STK10, BMPR2, MAP4K1, TM9A, BRAGD, CMPK1, IRAK4, INO, DYRK2, UBE2D1, ENTPD1, RUNX1, HELLS, CSF1R, ECRGL, TRP53, EEF1A1, OBSDN, ADSSL1, RAB8A, RAB8B, MYO1C, AKI, EEF1A2, MYO1G, ATAD2, BRIP1, MYO1F, DOCK8, PSMB8, MMAB, ABCB4, IKKBE, P2RX4, DNA2, PLK4, P2RX6, PLK3, PLK2, UULK1, UULK2, NDUFPV1, NDUFPV2, RHOT2, MYH13, RAP1B, MERTK, PIP4K2A, KIF23, KIF22, ACOX1, D2HGDH, ATL2, FIGL1, SLPN9, ATL3, PEX6, PIP5K2, PIP5K1, PINK1, SLPN8, RHOD, SLPN8, FES, RHOF, SLPN4, SLPN2, ACVR1B, GSK, RHOD, RHOC, CSK, SUCLA2, TUBA1A, TUBA1B, TUBA1C, RHOG, CDK14, ATPB8A, RHOF, PRKCA, ACADM, HSP90A1, KIF11, LIMK1, ACAD5, MCM3, UBE2C, CDK4, PRKCD, MCM4, UBE2B, CDK2, MCM5, PRKCB, MCM6, ARL3, ACADV, MFN2, KIF1C, MFN1, ATP6V1A, ACVR2B, RRA52, H2-AA, BUB1B, CAMK1D, CAMK2G, DCK, THBS1, ASNS, NAIP2, KIF4, TAP1, UCK2, HSPA5, EH01, CAMK2A, DCLK1, EH04, ACTB, ALPK1, HCK, ABCA8B, ABCA8A, GAS7, SIRT7, SMC2, SMCA, HSP90B1, CYBB, TEPI1, JAK2, APAF1, H2-DMA, ATRB1	1524	2183	13288	1.34	2.04E-06	4.07E-07	2.59E-06
GOTERM_MF_FAT	GO:0000166-nucleotide binding	335	15.57	1.59E-09	KIFC1, ADCY7, TUBB2B, TUBB2A, LDHG, PRKX, BTK, ACTG1, RAB28, OASL2, OASL1, MAP3K8, PRK3G, SUCLG1, MYH2, MYLK2, WNK2, GEM, MYH5, MYH8, RFC5, RND3, MAPK6, NME1, DID, PDGFRA, RAB12, MAPK7, S4304S522R1K, ACADSB, GNAI3, GNAI2, NEK2, PFKFB3, PFKFB1, STK17B, CHEK1, ARF6, MYO9B, OAS2, NAGK, HADHA, HSPA1L, MUSK, RAC2, IQH2, PAPBFL, BDNF, GCDH, GPD1, KIF8B, SPHK1, ARCG3, ATP13A1, VDAC1, ARCG1, VDAC1, ATP13A4, HYOU1, ATP2A2, ARF3, ARF4, TNF2, HSPA1A, ACAD11, CLCNK, SLC7A1, SPOT, BCKDK, RAB5C, KCN1J1, CAMK2K, CKB, ACTR3, MCC2, MCC1, TUBB8, TUBB6, MASTL, DOCK10, SIK1, TOP2A, DOCK11, TARSL2, RAP2B, CDC7, CDC6, RAP2A, LYN, PHKG1, RAB48, NDUFA13, PDCCC, 1700017808R1K, NDUFA10, MAST1, DNAC27, GM12250, SQLE, ADR, RIFP1, EF4A1, MAP3K10, STEAP2, ARL4C, MYO5A, ALDH5A1, UGDH, POA1, HK1, GALK2, RAB4A, RAB43, PTK2B, ABCD2, BUB1, CERK, PRKAA2, KIF21B, ETFA, ACUL5, MYO5C, PKD2, NOS1, FDK3, ACV1, NADK, NRP2, ATP1A1, APRT, SDHA, RPS6KA5, RAB22, NRAS, ABCC9, RAB31, MAPK12, ADCY9, PYGL, RAB3A, HSPA4L, KIF20B, PHGDH, ARCC3, CHTF18, GYK, AACS, GNA13, RNASEL, DSERT0579E, HMGCR, RBBM5, F13A1, RABD, RAB28, MYTHD1L, PPKAR2B, ACS1, IDH3G, ORLH, GBP10, RABL, MUK1, SARIE, MX1, NSR, MYAT, CITA, MAP4K4, RIFP2, OAS1A, PCB, PCB, SHN1, FGR, STK10, BMPR2, MAP4K1, TM9A, BRAGD, CMPK1, IRAK4, INO, DYRK2, UBE2D1, ENTPD1, RUNX1, HELLS, CSF1R, ECRGL, TRP53, EEF1A1, OBSDN, ADSSL1, RAB8A, RAB8B, MYO1C, AKI, EEF1A2, MYO1G, ATAD2, BRIP1, MYO1F, DOCK8, PSMB8, MMAB, ABCB4, IKKBE, P2RX4, DNA2, PLK4, P2RX6, PLK3, PLK2, UULK1, UULK2, NDUFPV1, NDUFPV2, RHOT2, MYH13, RAP1B, MERTK, PIP4K2A, KIF23, KIF22, ACOX1, D2HGDH, ATL2, FIGL1, SLPN9, ATL3, PEX6, PIP5K2, PIP5K1, PINK1, SLPN8, RHOD, SLPN8, FES, RHOF, SLPN4, SLPN2, ACVR1B, GSK, RHOD, RHOC, CSK, SUCLA2, TUBA1A, TUBA1B, TUBA1C, RHOG, CDK14, ATPB8A, RHOF, PRKCA, ACADM, HSP90A1, KIF11, LIMK1, ACAD5, MCM3, UBE2C, CDK4, PRKCD, MCM4, UBE2B, CDK2, MCM5, PRKCB, MCM6, ARL3, ACADV, MFN2, KIF1C, MFN1, ATP6V1A, ACVR2B, RRA52, H2-AA, BUB1B, CAMK1D, CAMK2G, DCK, THBS1, ASNS, NAIP2, KIF4, TAP1, UCK2, HSPA5, EH01, CAMK2A, DCLK1, EH04, ACTB, ALPK1, HCK, ABCA8B, ABCA8A, GAS7, SIRT7, SMC2, SMCA, HSP90B1, CYBB, TEPI1, JAK2, APAF1, H2-DMA, ATRB1	1524	2183	13288	1.34	2.04E-06	4.07E-07	2.59E-06
					KIFC1, ADCY7, TUBB2B, TUBB2A, LDHG, PRKX, BTK, ACTG1, RAB28, OASL2, OASL1, MAP3K8, PRK3G, SUCLG1, MYH2, MYLK2, WNK2, GEM, MYH5, MYH8, RFC5, RND3, MAPK6, NME1, DID, PDGFRA, RAB12, MAPK7, S4304S522R1K, ACADSB, GNAI3, GNAI2, NEK2, PFKFB3, PFKFB1, STK17B, CHEK1, ARF6, MYO9B, OAS2, NAGK, HADHA, HSPA1L, MUSK, RAC2, IQH2, PAPBFL, BDNF, GCDH, GPD1, KIF8B, SPHK1, ARCG3, ATP13A1, VDAC1, ARCG1, VDAC1, ATP13A4, HYOU1, ATP2A2, ARF3, ARF4, TNF2, HSPA1A, ACAD11, CLCNK, SLC7A1, SPOT, BCKDK, RAB5C, KCN1J1, CAMK2K, CKB, ACTR3, MCC2, MCC1, TUBB8, TUBB6, MASTL, DOCK10, SIK1, TOP2A, DOCK11, TARSL2, RAP2B, CDC7, CDC6, RAP2A, LYN, PHKG1, RAB48, NDUFA13, PDCCC, 1700017808R1K, NDUFA10, MAST1, DNAC27, GM12250, SQLE, ADR, RIFP1, EF4A1, MAP3K10, STEAP2, ARL4C, MYO5A, ALDH5A1, UGDH, POA1, HK1, GALK2, RAB4A, RAB43, PTK2B, ABCD2, BUB1, CERK, PRKAA2, KIF21B, ETFA, ACUL5, MYO5C, PKD2, NOS1, FDK3, ACV1, NADK, NRP2, ATP1A1, APRT, SDHA, RPS6KA5, RAB22, NRAS, ABCC9, RAB31, MAPK12, ADCY9, PYGL, RAB3A, HSPA4L, KIF20B, PHGDH, ARCC3, CHTF18, GYK, AACS, GNA13, RNASEL, DSERT0579E, HMGCR, RBBM5, F13A1, RABD, RAB28, MYTHD1L, PPKAR2B, ACS1, IDH3G, ORLH, GBP10, RABL, MUK1, SARIE, MX1, NSR, MYAT, CITA, MAP4K4, RIFP2, OAS1A, PCB, PCB, SHN1, FGR, STK10, BMPR2, MAP4K1, TM9A, BRAGD, CMPK1, IRAK4, INO, DYRK2, UBE2D1, ENTPD1, RUNX1, HELLS, CSF1R, ECRGL, TRP53, EEF1A1, OBSDN, ADSSL1, RAB8A, RAB8B, MYO1C, AKI, EEF1A2, MYO1G, ATAD2, BRIP1, MYO1F, DOCK8, PSMB8, MMAB, ABCB4, IKKBE, P2RX4, DNA2, PLK4, P2RX6, PLK3, PLK2, UULK1, UULK2, NDUFPV1, NDUFPV2, RHOT2, MYH13, RAP1B, MERTK, PIP4K2A, KIF23, KIF22, ACOX1, D2HGDH, ATL2, FIGL1, SLPN9, ATL3, PEX6, PIP5K2, PIP5K1, PINK1, SLPN8, RHOD, SLPN8, FES, RHOF, SLPN4, SLPN2, ACVR1B, GSK, RHOD, RHOC, CSK, SUCLA2, TUBA1A, TUBA1B, TUBA1C, RHOG, CDK14, ATPB8A, RHOF, PRKCA, ACADM, HSP90A1, KIF11, LIMK1, ACAD5, MCM3, UBE2C, CDK4, PRKCD, MCM4, UBE2B, CDK2, MCM5, PRKCB, MCM6, ARL3, AC							

						KIFC1, ADCY7, TUBB2B, TUBB2A, PRKX, BTK, ACTG1, OASL2, OASL1, MAP3K8, PIK3CG, SUGLG1, MYH2, MYLK2, WNK2, GEM, MYH9, MYH8, RFCS, RND3, MAPK6, NME1, PDGFRA, RAB12, MAPK7, S4S4S5S23R, DNAA5, DNAD2, PPF8E1, NKX2, PFKFB1, STX17B, CHEK1, MYO9B, ADRP, ADRP, OAS2, NAGK, HSPA1A, MUSK, RAC2, DHX58, KIF3B, SPHK1, ABCG3, ATP13A3, ABCG1, ATP13A4, HYOU1, ATP2A2, ARF4, ARF4, TNK2, HSPA13, CLCN5, SPG7, BCKDK, RAB5C, KCN11, CAMKK2, CK8, ACTR3, ACTR2, MCCC2, MCCC1, TUBB8, TUBB6, MAST1, DOCK10, SKI1, TOP2A, DOCK11, TABS12, RAP2B, CDC7, RAP2A, CDC4, LYN, PHKG1, RABH, NDUFA13, PDCC, 17005178D9HK, NDUFA10, MAST3, DNAC27, DN12250, ADK, RIKP1, EFPA1, MAP3K10, ARLC, MYO5A, ALDH18A1, HK1, GALX2, RABBA, RAB43, PTK2B, ABCD2, BUB1, CERK, PRKAA2, KIF21B, ACSL5, MYO5C, PDK2, PDK3, ACV1, NADK, ATP1A1, NPR2, APRT, RPS6KA5, RAB32, NRAS, ARCC9, RAB13, ADCY9, MAPK12, RAB3A, HSPA4L, KIF20B, ARCC3, CHTF18, GYK, AAC5, GNA13, RNASEL, DSERTD579E, F13A1, RHAD, PAK4B, MYTHD11, PRKAR2B, ACS31, DH3G, OPLAH, GBI10, RADL, MLKL, SARL8, MSL1, INSR, MATX, CITA, MAPK4A, RPK3, OAS1A, PCCB, PCCA, SRON1, FGR, STK10, BMPR2, MAP4K1, TMPA, BRAGO, CMPK1, IRAK4, DYRK2, UBE2D1, ENTPO1, RUNK1, HELLS, CSF1R, ERCC6L, TRP53, EEF1A1, OBSN, RABBA, ADO5L1, RAB8B, MYO1C, AK1, EEF1A2, MYO1G, ATAD2, BRP1, MYO1F, DOCK8, PSMB8, MMAB, ABCB4, IKKKE, P2RX4, DNA2, PLK4, P2RX6, PLK3, PLK2, UXL1, UXL2, MYH13, MERTK, PIPK4A, KIF23, KIF22, ATG12, D2HGDN, FIGNL1, SLPN, PK6, PPFPSK2, PPFPSK1, PINK1, RHOQ, SLPN8, FES, SLPN4, SLPN2, ACVR1B, RHO, SUCLA2, CSK, CDK14, ATP8A, PRKCA, HSP90AA1, KIF11, ACADM, ACADS, ULMK1, MCM3, CDK4, UBE2C, UBE2B, MCM4, PRKCD, CDK2, MCM5, PRKCB, MCM6, ACADVL, KIF1C, ATP6V1A, ACVR2B, BUB1B, H2-AA, CAMK10, CAMK2G, CDK, TRB3, ASNS, NAIP2, KIF4, TAP1, UCK2, HSPA5, EHD1, CAMK2A, DCL1, EHD4, ACTB, ALPK1, ABCAB8, HCK, ABCA8A, SMCA, CYBB, HSP90B1, TEP1, JAK2, APAF1, H2-DMA, ATP9A1	1524	1796	13288	1.34	8.33E-05	9.26E-06	1.06E-04
GOTERM_MF_FAT	GO:0032555-purine ribonucleotide binding	276	12.83	6.49E-08		KIFC1, ADCY7, LDHD, PRKX, BTK, ACTG1, OASL2, OASL1, MAP3K8, PIK3CG, MYH2, MYLK2, WNK2, MYH9, MYH8, RFCS, MAPK6, NME1, DLD, PDGFRA, MAPK7, ACAD5B, PFKFB1, NKX2, PFKFB1, STX17B, CHEK1, MYO9B, OAS2, NAGK, HSPA1A, MUSK, DHX58, GCDH, KIF3B, SPHK1, ABCG3, ATP13A3, ABCG1, ATP13A4, HYOU1, ATP2A2, HSPA13, TNK2, ACAD11, CLCN5, SPG7, BCKDK, KCN11, CAMKK2, CK8, ACTR3, ACTR2, MCCC2, MCCC1, MAST1, SKI1, TOP2A, TABS12, CDC7, CDC4, LYN, PHKG1, NDUFA13, PDCC, NDUFA10, MAST3, SGL1, RIKP1, ADK, EFPA1, MAP3K10, STEAP2, MYO5A, ALDH18A1, HK1, GALX2, PTK2B, ABCD2, BUB1, CERK, PRKAA2, KIF21B, MYO5C, ACSL5, ETTA, PKD2, NOS1, PDK3, ACV1, ATP1A1, NPR2, NADK, APRT, SDHA, RPS6KA5, ARCC9, ADCY9, MAPK12, HSPA4L, ARCC3, KIF20B, CHTF18, GYK, AAC5, RNASEL, DSERTD579E, F13A1, PHK2B, MYTHD11, PRKAR2B, ACS31, DH3G, OPLAH, MLKL, INSR, MATX, CITA, MAPK4A, RPK3, OAS1A, PCCB, PCCA, SKXN1, FGR, STK10, BMPR2, MAPK4A, TMPA, CMPK1, IRAK4, IVD, DYRK2, ENTPO1, RUNK1, UBE2D1, HELLS, CSF1R, ERCC6L, TRP53, OBSN, MYO1C, AK1, MYO1G, MYO1F, ATAD2, BRP1, MMAB, PSMB8, ABCB4, P2RX4, DNA2, IKKKE, PLK4, PLK3, P2RX6, PLK2, UXL1, UXL2, MYH13, MERTK, PIPK4A, KIF23, KIF22, ACOK1, D2HGDN, FIGNL1, SLPN, PK6, PPFPSK2, PPFPSK1, PINK1, SLPN8, FES, SLPN4, SLPN2, ACVR1B, GSK, SUCLA2, CSK, CDK14, ATP8A, PRKCA, HSP90AA1, KIF11, ACADM, ACADS, ULMK1, MCM3, CDK4, UBE2C, UBE2B, MCM4, PRKCD, CDK2, MCM5, PRKCB, MCM6, ACADVL, KIF1C, ATP6V1A, ACVR2B, BUB1B, H2-AA, CAMK10, CAMK2G, CDK, TRB3, ASNS, NAIP2, KIF4, TAP1, UCK2, HSPA5, EHD1, CAMK2A, DCL1, EHD4, ACTB, ALPK1, ABCAB8, HCK, ABCA8A, SMCA, CYBB, HSP90B1, TEP1, JAK2, APAF1, H2-DMA, ATP9A1	1524	1535	13288	1.32	4.46E-03	3.19E-04	5.67E-03
GOTERM_MF_FAT	GO:0035554-adenyl nucleotide binding	232	10.79	3.48E-08		KIFC1, ADCY7, LDHD, PRKX, BTK, ACTG1, OASL2, OASL1, MAP3K8, PIK3CG, MYH2, MYLK2, WNK2, MYH9, MYH8, RFCS, MAPK6, NME1, DLD, PDGFRA, MAPK7, ACAD5B, PFKFB1, NKX2, PFKFB1, STX17B, CHEK1, MYO9B, OAS2, NAGK, HSPA1A, MUSK, DHX58, GCDH, KIF3B, SPHK1, ABCG3, ATP13A3, ABCG1, ATP13A4, HYOU1, ATP2A2, HSPA13, TNK2, ACAD11, CLCN5, SPG7, BCKDK, KCN11, CAMKK2, CK8, ACTR3, ACTR2, MCCC2, MCCC1, MAST1, SKI1, TOP2A, TABS12, CDC7, CDC4, LYN, PHKG1, NDUFA13, PDCC, NDUFA10, MAST3, SGL1, RIKP1, ADK, EFPA1, MAP3K10, STEAP2, MYO5A, ALDH18A1, HK1, GALX2, PTK2B, ABCD2, BUB1, CERK, PRKAA2, KIF21B, MYO5C, ACSL5, ETTA, PKD2, NOS1, PDK3, ACV1, ATP1A1, NPR2, NADK, APRT, SDHA, RPS6KA5, ARCC9, ADCY9, MAPK12, HSPA4L, ARCC3, KIF20B, CHTF18, GYK, AAC5, RNASEL, DSERTD579E, F13A1, PHK2B, MYTHD11, PRKAR2B, ACS31, DH3G, OPLAH, MLKL, INSR, MATX, CITA, MAPK4A, RPK3, OAS1A, PCCB, PCCA, SKXN1, FGR, STK10, BMPR2, MAPK4A, TMPA, CMPK1, IRAK4, IVD, DYRK2, ENTPO1, RUNK1, UBE2D1, HELLS, CSF1R, ERCC6L, TRP53, OBSN, MYO1C, AK1, MYO1G, MYO1F, ATAD2, BRP1, MMAB, PSMB8, ABCB4, P2RX4, DNA2, IKKKE, PLK4, PLK3, P2RX6, PLK2, UXL1, UXL2, MYH13, MERTK, PIPK4A, KIF23, KIF22, ACOK1, D2HGDN, FIGNL1, SLPN, PK6, PPFPSK2, PPFPSK1, PINK1, SLPN8, FES, SLPN4, SLPN2, ACVR1B, GSK, SUCLA2, CSK, CDK14, ATP8A, PRKCA, HSP90AA1, KIF11, ACADM, ACADS, ULMK1, MCM3, CDK4, UBE2C, UBE2B, MCM4, PRKCD, CDK2, MCM5, PRKCB, MCM6, ACADVL, KIF1C, ATP6V1A, ACVR2B, BUB1B, H2-AA, CAMK10, CAMK2G, CDK, TRB3, ASNS, NAIP2, KIF4, TAP1, UCK2, HSPA5, EHD1, CAMK2A, DCL1, EHD4, ACTB, ALPK1, ABCAB8, HCK, ABCA8A, SMCA, CYBB, HSP90B1, TEP1, JAK2, APAF1, H2-DMA, ATP9A1	1524	1548	13288	1.31	8.27E-03	5.19E-04	1.05E-02
GOTERM_BP_FAT	GO:0001883-purine nucleotide binding	232	10.79	6.47E-08		KIFC1, ADCY7, LDHD, PRKX, BTK, ACTG1, OASL2, OASL1, MAP3K8, PIK3CG, MYH2, MYLK2, WNK2, MYH9, MYH8, RFCS, MAPK6, NME1, DLD, PDGFRA, MAPK7, ACAD5B, PFKFB1, NKX2, PFKFB1, STX17B, CHEK1, MYO9B, OAS2, NAGK, HSPA1A, MUSK, DHX58, GCDH, KIF3B, SPHK1, ABCG3, ATP13A3, ABCG1, ATP13A4, HYOU1, ATP2A2, HSPA13, TNK2, ACAD11, CLCN5, SPG7, BCKDK, KCN11, CAMKK2, CK8, ACTR3, ACTR2, MCCC2, MCCC1, MAST1, SKI1, TOP2A, TABS12, CDC7, CDC4, LYN, PHKG1, NDUFA13, PDCC, NDUFA10, MAST3, SGL1, RIKP1, ADK, EFPA1, MAP3K10, STEAP2, MYO5A, ALDH18A1, HK1, GALX2, PTK2B, ABCD2, BUB1, CERK, PRKAA2, KIF21B, MYO5C, ACSL5, ETTA, PKD2, NOS1, PDK3, ACV1, ATP1A1, NPR2, NADK, APRT, SDHA, RPS6KA5, ARCC9, ADCY9, MAPK12, HSPA4L, ARCC3, KIF20B, CHTF18, GYK, AAC5, RNASEL, DSERTD579E, F13A1, PHK2B, MYTHD11, PRKAR2B, ACS31, DH3G, OPLAH, MLKL, INSR, MATX, CITA, MAPK4A, RPK3, OAS1A, PCCB, PCCA, SKXN1, FGR, STK10, BMPR2, MAPK4A, TMPA, CMPK1, IRAK4, IVD, DYRK2, ENTPO1, RUNK1, UBE2D1, HELLS, CSF1R, ERCC6L, TRP53, OBSN, MYO1C, AK1, MYO1G, MYO1F, ATAD2, BRP1, MMAB, PSMB8, ABCB4, P2RX4, DNA2, IKKKE, PLK4, PLK3, P2RX6, PLK2, UXL1, UXL2, MYH13, MERTK, PIPK4A, KIF23, KIF22, ACOK1, D2HGDN, FIGNL1, SLPN, PK6, PPFPSK2, PPFPSK1, PINK1, SLPN8, FES, SLPN4, SLPN2, ACVR1B, GSK, SUCLA2, CSK, CDK14, ATP8A, PRKCA, HSP90AA1, KIF11, ACADM, ACADS, ULMK1, MCM3, CDK4, UBE2C, UBE2B, MCM4, PRKCD, CDK2, MCM5, PRKCB, MCM6, ACADVL, KIF1C, ATP6V1A, ACVR2B, BUB1B, H2-AA, CAMK10, CAMK2G, CDK, TRB3, ASNS, NAIP2, KIF4, TAP1, UCK2, HSPA5, EHD1, CAMK2A, DCL1, EHD4, ACTB, ALPK1, ABCAB8, HCK, ABCA8A, SMCA, CYBB, HSP90B1, TEP1, JAK2, APAF1, H2-DMA, ATP9A1	1524	1558	13288	1.30	9.06E-03	5.35E-04	1.16E-02
GOTERM_BP_FAT	GO:0004802-antigen processing and presentation of peptide antigen	19	0.88	1.01E-08		H2-M3, H2-D1, UNC93B1, 2610524H68IK, IF30, H2-DMB1, H2-AB1, CALR, FCGR1, CD74, FCGR3, B2M, SLC11A1, FCGR2B, H2-EB1, FCER1G, H2-AA, MHL, H2-DMA	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002478-antigen processing and presentation of exogenous peptide antigen	15	0.70	2.56E-08		H2-M3, UNC93B1, 2610524H68IK, IF30, H2-DMB1, H2-AB1, FCGR1, CD74, FCGR3, B2M, FCGR2B, H2-EB1, FCER1G, H2-AA, H2-DMA	1594	35	13588	4.63	3.68E-05	2.45E-06	1.86E-05
GOTERM_BP_FAT	GO:0019884-antigen processing and presentation of exogenous antigen	15	0.70	7.11E-07		H2-M3, UNC93B1, 2610524H68IK, IF30, H2-DMB1, H2-AB1, FCGR1, CD74, FCGR3, B2M, FCGR2B, H2-EB1, FCER1G, H2-AA, H2-DMA	1594	23	13588	5.56	9.39E-05	4.91E-06	4.72E-05
GOTERM_BP_FAT	GO:0002495-antigen processing and presentation of peptide antigen via MHC class II	11	0.51	1.96E-06		FCGR2B, H2-EB1, UNC93B1, 2610524H68IK, H2-AA, FCER1G, H2-DMB1, IF30, H2-AB1, H2-DMA, CD74	1594	16	13588	5.86	7.10E-03	1.93E-04	3.60E-03
GOTERM_BP_FAT	GO:0019886-antigen processing and presentation of exogenous peptide antigen via MHC class II	11	0.51	1.96E-06		FCGR2B, H2-EB1, UNC93B1, 2610524H68IK, H2-AA, FCER1G, H2-DMB1, IF30, H2-AB1, H2-DMA, CD74	1594	16	13588	5.86	7.10E-03	1.93E-04	3.60E-03
GOTERM_BP_FAT	GO:0002504-antigen processing and presentation of peptide or polysaccharide antigen via MHC class I	11	0.51	1.62E-05		FCGR2B, H2-EB1, UNC93B1, 2610524H68IK, H2-AA, FCER1G, H2-DMB1, IF30, H2-AB1, H2-DMA, CD74	1594	19	13588	4.94	5.72E-02	1.02E-03	2.98E-02
Annotation Cluster 5 Category	Enrichment Score: 5.855933634213578 Term	Count %	PValue	Genes		CYBB3, NDUFB3, NDUFB5, GMPF2, NC72, NDUFB8, NC71, NDUFA13, GMPF, ECOT, NDUFAF1, POR, NDUFA12, NDUFS7, GSR, NDUFA4, NDUFV1, NDUFB8, NDUFV2, DLD, NDUFS3, NDUFS2, NDUFS1, NDUFB3, NDUFB8, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS4, NDUFV1, NDUFV2, NDUFS8, NDUFS3, NDUFS2, NDUFS1	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0004802-antigen processing and presentation of peptide antigen	23	1.07	9.98E-09		CYBB3, NDUFB3, NDUFB5, GMPF2, NC72, NDUFB8, NC71, NDUFA13, GMPF, ECOT, NDUFAF1, POR, NDUFA12, NDUFS7, GSR, NDUFA4, NDUFV1, NDUFB8, NDUFV2, DLD, NDUFS3, NDUFS2, NDUFS1, NDUFB3, NDUFB8, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS4, NDUFV1, NDUFV2, NDUFS8, NDUFS3, NDUFS2, NDUFS1	1524	51	13288	3.93	1.28E-05	1.83E-06	1.63E-05
GOTERM_BP_FAT	GO:0003954-NADH dehydrogenase activity	13	0.60	3.55E-06		NDUFS3, NDUFS2, NDUFS1	1524	24	13288	4.72	4.55E-03	3.04E-04	5.78E-03
GOTERM_BP_FAT	GO:0050136-NADH dehydrogenase (quinone) activity	13	0.60	3.55E-06		NDUFS3, NDUFS2, NDUFS1	1524	24	13288	4.72	4.55E-03	3.04E-04	5.78E-03
GOTERM_MF_FAT	GO:0008137-NADH dehydrogenase (ubiquinone) activity	13	0.60	3.55E-06		NDUFS3, NDUFS2, NDUFS1	1524	24	13288	4.72	4.55E-03	3.04E-04	5.78E-03
GOTERM_MF_FAT	GO:0016655-oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acce	13	0.60	1.64E-05		NDUFS3, NDUFS2, NDUFS1	1524	27	13288	4.20	2.08E-02	9.15E-04	2.67E-02
Annotation Cluster 6 Category	Enrichment Score: 5.827203670584949 Term	Count %	PValue	Genes		UNC93B1, NDUFB3, NDUFB5, GMPF2, NC72, NDUFB8, NC71, NDUFA13, GMPF, ECOT, NDUFAF1, POR, NDUFA12, NDUFS7, GSR, NDUFA4, NDUFV1, NDUFB8, NDUFV2, DLD, NDUFS3, NDUFS2, NDUFS1, NDUFB3, NDUFB8, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS4, NDUFV1, NDUFV2, NDUFS8, NDUFS3, NDUFS2, NDUFS1	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0045333-cellular respiration	25	1.16	1.38E-08		UNC93B1, NDUFB3, NDUFB5, GMPF2, NC72, NDUFB8, NC71, NDUFA13, GMPF, ECOT, NDUFAF1, POR, NDUFA12, NDUFS7, GSR, NDUFA4, NDUFV1, NDUFB8, NDUFV2, DLD, NDUFS3, NDUFS2, NDUFS1, NDUFB3, NDUFB8, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS4, NDUFV1, NDUFV2, NDUFS8, NDUFS3, NDUFS2, NDUFS1	1594	59	13588	3.61	5.04E-05	2.96E-06	2.55E-05
GOTERM_BP_FAT	GO:0051187-collector catabolic process	17	0.79	1.13E-07		ALDH1L1, NC72, NC71, SUCLG1, CS, IDH3B, IDH3A, SDHA, SDHB, IDH3G, SDHC, HMOX1, IDH2, ALDH1L1, NC72, NC71, SUCLG1, CS, IDH3B, IDH3A, SDHA, SDHB, IDH3G, SDHC, IDH2, 2610507811RK, FHL1, SUCLA2, MDH1	1594	32	13588	4.53	4.11E-04	1.71E-05	2.08E-04
GOTERM_BP_FAT	GO:0009109-coenzyme catabolic process	16	0.74	1.59E-07		FHL1, SUCLA2, MDH1	1594	29	13588	4.70	5.77E-04	2.22E-05	9.92E-04
GOTERM_BP_FAT	GO:0006084-acetyl-CoA metabolic process	16	0.74	4.89E-07		SUCLG1, CS, IDH3B, ACV1, DLAT, IDH3A, SDHA, SDHB, ACS1, IDH3G, SDHC, IDH2, 2610507811RK, FHL1, SUCLA2, MDH1	1594	31	13588	4.40	1.78E-03	6.36E-05	9.00E-04
GOTERM_BP_FAT	GO:0006099-tricarboxylic acid cycle	13	0.60	2.53E-06		SUCLG1, CS, IDH3B, IDH3A, SDHA, SDHB, IDH3G, SDHC, IDH2, 2610507811RK, FHL1, SUCLA2, MDH1	1594	23	13588	4.82	9.15E-03	2.14E-04	4.65E-03
GOTERM_BP_FAT	GO:0046356-acetyl-CoA catabolic process	13	0.60	4.51E-06		SUCLG1, CS, IDH3B, IDH3A, SDHA, SDHB, IDH3G, SDHC, IDH2, 2610507811RK, FHL1, SUCLA2, MDH1	1594	24	13588	4.62	1.63E-02	3.42E-04	8.30E-03
GOTERM_BP_FAT	GO:0009060-aerobic respiration	13	0.60	2.07E-05		SUCLG1, CS, IDH3B, IDH3A, SDHA, SDHB, IDH3G, SDHC, IDH2, 2610507811RK, FHL1, SUCLA2, MDH1	1594	27	13588	4.10	7.26E-02	1.28E-03	3.81E-02
Annotation Cluster 7 Category	Enrichment Score: 5.64349383324884 Term	Count %	PValue	Genes		UNC93B1, NDUFB3, NDUFB5, GMPF2, NC72, NDUFB8, NC71, NDUFA13, GMPF, ECOT, NDUFAF1, POR, NDUFA12, NDUFS7, GSR, NDUFA4, NDUFV1, NDUFB8, NDUFV2, DLD, NDUFS3, NDUFS2, NDUFS1, NDUFB3, NDUFB8, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS4, NDUFV1, NDUFV2, NDUFS8, NDUFS3, NDUFS2, NDUFS1	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042330-taxis	36	1.67	1.25E-08		NR2P, CSAR1, CCL2, CYS1TR1, S100A8, CCR1, C13L3, SLC37A4, S100A9, CCL9, CCR2, PF4, ITGB2, CCL4, ITGAM, CCL6, DOCK2, EARM, RAC2, CXCL, CSF3R, IL1B, FCER1G, PRKCA, CSAR1, FCGR3, 2610507811RK, FHL1, SUCLA2, MDH1	1594	109	13588	2.82	4.54E-05	2.84E-06	2.30E-05
GOTERM_BP_FAT	GO:0005995-leukocyte chemotaxis	36	1.67	1.25E-08		NR2P, CSAR1, CCL2, CYS1TR1, S100A8, CCR1, C13L3, SLC37A4, S100A9, CCL9, CCR2, PF4, ITGB2, CCL4, ITGAM, CCL6, DOCK2, EARM, RAC2, CXCL, CSF3R, IL1B, FCER1G, PRKCA, CSAR1, FCGR3, 2610507811RK, FHL1, SUCLA2, MDH1	1594	109	13588	2.82	4.54E-05	2.84E-06	2.30E-05
GOTERM_BP_FAT	GO:0006032-cell chemotaxis	15	0.70	3.98E-07		IL1B, CSF3R	1594	27	13588	4.74	1.45E-03	5.77E-05	7.33E-04
Annotation Cluster 8 Category	Enrichment Score: 5.130596702981142 Term	Count %	PValue	Genes		NR2P, CSAR1, CCL2, CYS1TR1, S100A8, CCR1, C13L3, SLC37A4, S100A9, CCL9, CCR2, PF4, ITGB2, CCL4, ITGAM, CCL6, DOCK2, EARM, RAC2, CXCL, CSF3R, IL1B, FCER1G, PRKCA, CSAR1, FCGR3, 2610507811RK, FHL1, SUCLA2, MDH1	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001775-cell activation	67	3.11	4.70E-11		DNAA1, HPRY, ELTA, STAT5B, PTPN22, TLR4, MYD88, TRAF2, IRAK4, TRAF6, TRAF7, TRAF8, TRAF9, TRAF10, TRAF11, TRAF12, TRAF13, TRAF14, TRAF15, TRAF16, TRAF17, TRAF18, TRAF19, TRAF20, TRAF21, TRAF22, TRAF23, TRAF24, TRAF25, TRAF26, TRAF27, TRAF28, TRAF29, TRAF30, TRAF31, TRAF32, TRAF33, TRAF34, TRAF35, TRAF36, TRAF37, TRAF38, TRAF39, TRAF40, TRAF41, TRAF42, TRAF43, TRAF44, TRAF45, TRAF46, TRAF47, TRAF48, TRAF49, TRAF50, TRAF51, TRAF52, TRAF53, TRAF54, TRAF55, TRAF56, TRAF57, TRAF58, TRAF59, TRAF60, TRAF61, TRAF62, TRAF63, TRAF64, TRAF65, TRAF66, TRAF67, TRAF68, TRAF69, TRAF70, TRAF71, TRAF72, TRAF73, TRAF74, TRAF75, TRAF76, TRAF77, TRAF78, TRAF79, TRAF80, TRAF81, TRAF82, TRAF83, TRAF84, TRAF85, TRAF86, TRAF87, TRAF88, TRAF89, TRAF90, TRAF91, TRAF92, TRAF93, TRAF94, TRAF95, TRAF96, TRAF97, TRAF98, TRAF99, TRAF100, TRAF101, TRAF102, TRAF103, TRAF104, TRAF105, TRAF106, TRAF107, TRAF108, TRAF109, TRAF110, TRAF111, TRAF112, TRAF113, TRAF114, TRAF115, TRAF116, TRAF117, TRAF118, TRAF119, TRAF120, TRAF121, TRAF122, TRAF123, TRAF124, TRAF125, TRAF126, TRAF127, TRAF128, TRAF129, TRAF130, TRAF131, TRAF132, TRAF133, TRAF134, TRAF135, TRAF136, TRAF137, TRAF138, TRAF139, TRAF140, TRAF141, TRAF142, TRAF143, TRAF144, TRAF145, TRAF146, TRAF147, TRAF148, TRAF149, TRAF150, TRAF151, TRAF152, TRAF153, TRAF154, TRAF155, TRAF156, TRAF157, TRAF158, TRAF159, TRAF160, TRAF161, TRAF162, TRAF163, TRAF164, TRAF165, TRAF166, TRAF167, TRAF168, TRAF169, TRAF170, TRAF171, TRAF172, TRAF173, TRAF174, TRAF175, TRAF176, TRAF177, TRAF178, TRAF179, TRAF180, TRAF181, TRAF182, TRAF183, TRAF184, TRAF185, TRAF186, TRAF187, TRAF188, TRAF189, TRAF190, TRAF191, TRAF192, TRAF193, TRAF194, TRAF195, TRAF196, TRAF197, TRAF198, TRAF199, TRAF200, TRAF201, TRAF202, TRAF203, TRAF204, TRAF205, TRAF206, TRAF207, TRAF208, TRAF209, TRAF210, TRAF211, TRAF212, TRAF213, TRAF214, TRAF215, TRAF216, TRAF217, TRAF218, TRAF219, TRAF220, TRAF221, TRAF222, TRAF223, TRAF224, TRAF225, TRAF226, TRAF227, TRAF228, TRAF229, TRAF230, TRAF231, TRAF232, TRAF233, TRAF234, TRAF235, TRAF236, TRAF237, TRAF238, TRAF239, TRAF240, TRAF241, TRAF242, TRAF243, TRAF244, TRAF245, TRAF246, TRAF247, TRAF248, TRAF249, TRAF250, TRAF251, TRAF252, TRAF253, TRAF254, TRAF255, TRAF256, TRAF257, TRAF258, TRAF259, TRAF260, TRAF261, TRAF262, TRAF263, TRAF264, TRAF265, TRAF266, TRAF267, TRAF268, TRAF269, TRAF270, TRAF271, TRAF272, TRAF273, TRAF274, TRAF275, TRAF276, TRAF277, TRAF278, TRAF279, TRAF280, TRAF281, TRAF282, TRAF283, TRAF284, TRAF285, TRAF286, TRAF287, TRAF288, TRAF289, TRAF290, TRAF291, TRAF292, TRAF293, TRAF294, TRAF295, TRAF296, TRAF297, TRAF298, TRAF299, TRAF300, TRAF301, TRAF302, TRAF303, TRAF304, TRAF305, TRAF306, TRAF307							



GOTERM_BP_FAT	GO:0045321-leukocyte activation	61	2.84	1.44E-10	HDACS, FCGR2B, SLC7A2, BAX, PLCG2, H2-DMA	1594	219	13588	2.37	5.23E-07	5.23E-08	2.64E-07
GOTERM_BP_FAT	GO:0046649-lymphocyte activation	50	2.32	6.88E-08	HPRT, ELFA, STAT5B, PTPN22, TP052, SKAP2, C8B8, TGFBI, CD48, CXCR4, WWP1, IMPDH1, RHOD, EGR1, SATB1, RELB, NFAM1, CD40, MYH9, PRKCD, WAS, IFNAR1, LAT2, CD86, UNC13D, LCP1, ITGAL, SPPI1, ITGB2, IL7R, ITGAM, ADA, CD74, SLC11A1, DOCK2, ITGAX, PPP3CB, BCL3, HELLS, BLNK, TRP53, EXO1, PTPRC, H2-M3, IKZF1, VAV1, HDACS, BAX, PLCG2, H2-DMA	1594	191	13588	2.23	2.50E-04	1.09E-05	1.27E-04
GOTERM_BP_FAT	GO:0032943-mononuclear cell proliferation	19	0.88	5.38E-07	ITGAX, CXCR4, BAX, IMPDH1, HELLS	1594	43	13588	3.77	1.95E-03	6.75E-05	9.89E-04
GOTERM_BP_FAT	GO:0070661-leukocyte proliferation	19	0.88	5.38E-07	ITGAX, CXCR4, BAX, IMPDH1, HELLS	1594	43	13588	3.77	1.95E-03	6.75E-05	9.89E-04
GOTERM_BP_FAT	GO:0046651-lymphocyte proliferation	18	0.84	1.96E-05	CXCR4, BAX, IMPDH1, HELLS	1594	42	13588	3.65	7.09E-03	1.98E-04	3.60E-03
GOTERM_BP_FAT	GO:0042110-T cell activation	33	1.53	2.37E-06	ITGAX, ELFA, STAT5B, PTPN22, ITGB2, IL7R, ITGAM, TGFBI, CD74, CD48, SLC11A1, DOCK2, ITGAX, CXCR4, WWP1, PPP3CB, BCL3, RHOD, EGR1, TRP53, PTPRC, SATB1, H2-M3, IKZF1, RELB, MYH9, WAS, VAV1, IFNAR1, CD86, BAX, H2-DMA, LCP1	1594	116	13588	2.43	8.58E-03	2.15E-04	4.35E-03
GOTERM_BP_FAT	GO:0048534-hemopoietic or lymphoid organ development	60	2.79	5.16E-02	GMP12, STAT5B, PTPN22, NFKB2, PRDX1, TP052, C8B8, TGFBI, ANK1, TNFRSF11A, WWP1, CASP8, RHOD, EGR1, SGP11, SATB1, FECH, LYN, RELB, NFAM1, MYH9, TACC3, DNASE2A, HF1A, IL18B3, VEGFA, CCR2, CCR1, SLC37A4, SFKN1, SPPI1, SONE, IL7R, CD74, ADA, MLF1, DOCK2, PPP3CB, BCL3, RUNX1, HELLS, CEBPA, TRP53, PTPRC, IKZF1, HCL31, BPGM, VAV1, SOD2, HDACS, PLSCR1, CNB2, ID2, CXCL13, BAX, PLCG2, IRF8, JAK2, H2-DMA	1594	281	13588	1.82	1.86E-02	3.83E-04	9.49E-03
GOTERM_BP_FAT	GO:0030097-hemopoiesis	55	2.56	6.08E-06	GMP12, STAT5B, PTPN22, NFKB2, PRDX1, TP052, C8B8, TGFBI, ANK1, WWP1, CASP8, RHOD, EGR1, SGP11, SATB1, FECH, LYN, RELB, NFAM1, MYH9, TACC3, DNASE2A, HF1A, IL18B3, VEGFA, CCR2, CCR1, SLC37A4, SFKN1, SPPI1, SONE, IL7R, CD74, ADA, MLF1, DOCK2, PPP3CB, BCL3, RUNX1, HELLS, CEBPA, TRP53, PTPRC, IKZF1, HCL31, BPGM, VAV1, SOD2, HDACS, PLSCR1, CNB2, ID2, CXCL13, BAX, PLCG2, IRF8, JAK2, H2-DMA	1594	251	13588	1.87	2.19E-02	4.34E-04	1.12E-02
GOTERM_BP_FAT	GO:0005250-immune system development	61	2.84	1.22E-05	PRKAG3, UQCRC1, PHH8, NDUFB8, PHKA1, SLC37A4, UQCRC11, GOT1, PPP1R3B, IDH3G, PPP1R1A, OYS1, IDH2, FH1, SUC1A2, NDUFB1, AGL, NDUFA5, PHN2, ALDH5A1, SUCGA1, EPM2A, CS, IDH3B, PPP1R3A, IDH3A, SOD2, SIDA, SLC25A12, SORH, SLC25A13, PVH1, SDHC, SLC37A2, DGL, SLC09B7B1, IRM, UQCRC1, C12orf65	1594	295	13588	1.76	4.33E-02	7.90E-04	2.24E-02
Annotation Cluster 10 Category	Enrichment Score: 4.73772267929924	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0015980-energy derivation by oxidation of organic compounds	39	1.81	5.03E-12	MDH1, PYGB	1594	98	13588	3.39	1.83E-08	3.66E-09	9.25E-09
Annotation Cluster 11 Category	Enrichment Score: 4.5444652420965435	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
GOTERM_MF_FAT	GO:0051015-actin filament binding	21	0.98	1.43E-07	PKNOX2, CORD1A, EZR, LASP1, AIF1, LUPRRC, LCP1, MYO5C	1524	49	13288	3.74	1.84E-04	1.84E-05	2.33E-04
Annotation Cluster 12 Category	Enrichment Score: 4.41429504097982	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0002250-adaptive immune response	27	1.26	2.00E-06	IL18, NFKB2, TLR6, C1QC, CD74, SLC11A1, MYD88, KLHL6, FCER1G, BCL3, NRP5D, EXO1, ICAM1, CFB, RELB, PRKCD, FCGRI, FCGRI3, C1QA, C1QB, UNC13D, FCGR2B, IL18B3, IRF7, VEGFA, H2-AA, H2-DMA	1594	84	13588	2.74	7.26E-03	1.92E-04	3.68E-03
GOTERM_BP_FAT	GO:0002460-adaptive immune response based on somatic recombination of immune receptors built fr	27	1.26	2.00E-06	IL18, NFKB2, TLR6, C1QC, CD74, SLC11A1, MYD88, KLHL6, FCER1G, BCL3, NRP5D, EXO1, ICAM1, CFB, RELB, PRKCD, FCGRI, FCGRI3, C1QA, C1QB, UNC13D, FCGR2B, IL18B3, IRF7, VEGFA, H2-AA, H2-DMA	1594	84	13588	2.74	7.26E-03	1.92E-04	3.68E-03
GOTERM_BP_FAT	GO:0002252-immune effector process	35	1.63	2.00E-06	BNIP1, IL7R, T147, C1QC, T148, CD74, SLC11A1, MYD88, KLHL6, FCER1G, BCL3, NRP5D, EXO1, ICAM1, CFB, PTPRC, PTPN6, ICAM1, CADM9, C7B, C7C1, SAMHD1, MYO1F, PRKCD, FCGRI, FCGRI3, C1QA, C1QB, ARCCD, LAT2, UNC13D, FCGR2B, IL18B3, IRF7, H2-AA, H2-DMA	1594	126	13588	2.37	7.26E-03	1.87E-04	3.68E-03
Annotation Cluster 13 Category	Enrichment Score: 4.305942935764653	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0016044-membrane organization	61	2.84	7.88E-07	CD209A, LDLR, HPIR, SORL1, BINP3, NRCAM, DAB2, API51, CTNN, NECA2, CAP1, GHR, DBNL, CDC88A, MYH2, LCAT2, SIRM, LDUARP1, ELMO1, TACC3, MYH9, FDN3, UHRF1, MAD2L1, RCC2, RNF1, STEAP2, ANAPC1, SGC4, STON2, BDT, PPT1, CD9, SLC11A1, DOCK2, FCGRI3, PTX3, IDH1, MRC1, TRP53, VAV3, HCN, LMCN, SUN2, STAB2, FCGRI, VAV1, FCGRI3, CORO1C, NRAS, KNNA4, LRPI, FCGR2B, UTK1, BAX, RAB3A, IRF8, CLEC7A, MERTK, CLCN5	1594	272	13588	1.91	2.86E-03	8.96E-05	1.45E-03
GOTERM_BP_FAT	GO:0006897-endocytosis	43	2.00	2.50E-05	STON2, CD209A, LDLR, HPIR, SORL1, PPT1, SLC11A1, DAB2, CTNN, API51, NECA2, FCGRI3, CAP1, ENO1, PTX3, GHR, NRC1, DBNL, NCK, STAB2, FCGRI, SIRM, VAV1, LDUARP1, FCGRI3, ELMO1, CORO1C, NRAS, LRP1, UNC13D, FCGR2B, UTK1, NME1, LRP12, RAB3A, IRF8, RIN1, CLEC7A, STEAP2, MERTK, ANKRY1, CLCN5	1594	188	13588	1.95	8.69E-02	1.46E-03	4.59E-02
GOTERM_BP_FAT	GO:0010324-membrane invagination	43	2.00	2.50E-05	STON2, CD209A, LDLR, HPIR, SORL1, PPT1, SLC11A1, DAB2, CTNN, API51, NECA2, FCGRI3, CAP1, ENO1, PTX3, GHR, NRC1, DBNL, NCK, STAB2, FCGRI, SIRM, VAV1, LDUARP1, FCGRI3, ELMO1, CORO1C, NRAS, LRP1, UNC13D, FCGR2B, UTK1, NME1, LRP12, RAB3A, IRF8, RIN1, CLEC7A, STEAP2, MERTK, ANKRY1, CLCN5	1594	188	13588	1.95	8.69E-02	1.46E-03	4.59E-02
Annotation Cluster 14 Category	Enrichment Score: 4.221758640992546	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0007049-cell cycle	120	5.58	9.58E-09	KIFC1, S100A6, PRC1, DBF4, PTTG1, FOXO4, CDC48, CUL7, INCENP, MAP3K8, ATF6B, CDCA2, MTUS1, CDCA3, PDPN, SGO2, SKP2, ESPL1, GPR132, PLK1S1, TACC3, MYH9, FDN3, UHRF1, MAD2L1, RCC2, MAPK6, ZWINT, STMN1, MAPK7, PP2R3A, NEK2, CHEK1, ANLN, CCNG1, SPC25, NCAPH2, TP02, FBXO5, SKA1, LFNG, HELLS, ERCC91, TRP53, CNAIP, CPG1, IKZF1, MNM2, AK1, BRC1, NOTCH2, CDKN1A, PLK3, PLK2, RGS2, FBXO31, CHAF1A, CHAF1B, E2F1, GAS2L3, E2F6, E2F8, CUL2D1, CDT1, CCN1, CDRF1, TUBB8, RANBP1, SKI, CDK7, CDCA, ARHGDF2, CCNK, KIF11, NUSAP1, 1700017805IRK, HMG2A, NCDA, CDK4, UBE2C, UBE2B, CDK2, JMY, NCAM, AKL3, RBBP9, MN2, CCND1, BUB1B, RBBM3B, GADD45A, CKS1B, CAMK2G, POLA1, MLF1, NCAPH, BUB1, PPP3CA, ZWILCH, CAMK2A, EXO1, BOD1, KATZB, NASP, ANXA1, BIRC5, SIRT7, RACGAP1, SMC2, RGS14, SMCA, RASSF4, CCNB2, MAPK12, RASP2, CKS2, PHGDH, KIF20B, GAS2L1, OHT18	1594	611	13588	1.67	3.49E-05	2.49E-06	1.76E-05
GOTERM_BP_FAT	GO:0000278-mitotic cell cycle	55	2.56	2.50E-05	KIFC1, E2F6, DBF4, PTTG1, FOXO4, CDC48, INCENP, ATF6B, TUBB8, CDCA2, RANBP1, CDCA3, CDC6, ARHGDF2, CCNK, KIF11, SGO2, SKP2, NUSAP1, GPR132, PLK1S1, MYH9, UBE2C, TACC3, HMG2A, UBE2B, CDK2, RBBP9, CCND1, MAD2L1, RCC2, ZWINT, BUB1B, STMN1, GADD45A, PP2R3A, NEK2, CAMK2G, POLA1, ANLN, CHEK1, CCNG1, SPC25, NCAPH, NCAPH2, BUB1, FBXO5, SKA1, PPP3CA, ZWILCH, LFNG, CAMK2A, HELLS, ERCC91, BOD1, BIRC5, SIRT7, SMC2, RGS14, SMCA, CCNB2, RASP2, KIF20B, GAS2L1, OHT18, PTTG1, FOXO4, CDC48, INCENP, ATF6B, TUBB8, CDCA2, RANBP1, CDCA3, CDC6, ARHGDF2, CCNK, KIF11, SGO2, SKP2, NUSAP1, E2F6, E2F8, CUL2D1, CDT1, CCN1, CDRF1, TUBB8, RANBP1, SKI, CDK7, CDCA, ARHGDF2, CCNK, KIF11, NUSAP1, 1700017805IRK, HMG2A, NCDA, CDK4, UBE2C, UBE2B, CDK2, JMY, NCAM, AKL3, RBBP9, MN2, CCND1, RORB1, RBBM3, GADD45A, PP2R3A, NEK2, CAMK2G, POLA1, ANLN, CHEK1, CCNG1, SPC25, NCAPH, NCAPH2, BUB1, FBXO5, SKA1, PPP3CA, ZWILCH, LFNG, CAMK2A, HELLS, ERCC91, EXO1, BOD1, MNM2, AK1, BIRC5, SIRT7, RACGAP1, SMC2, BRCAL, RGS14, SMCA, NOTCH2, CDKN1A, CCNB2, PHGDH, KIF20B, GAS2L1	1594	244	13588	1.92	9.05E-03	2.16E-04	4.59E-03
GOTERM_BP_FAT	GO:0022402-cell cycle process	78	3.63	3.25E-06	KIFC1, E2F6, DBF4, PTTG1, FOXO4, CDC48, INCENP, ATF6B, TUBB8, CDCA2, RANBP1, CDCA3, CDC6, ARHGDF2, CCNK, KIF11, SGO2, SKP2, NUSAP1, GPR132, PLK1S1, MYH9, UBE2C, TACC3, HMG2A, UBE2B, CDK2, RBBP9, CCND1, MAD2L1, RCC2, ZWINT, BUB1B, STMN1, GADD45A, PP2R3A, NEK2, CAMK2G, POLA1, ANLN, CHEK1, CCNG1, SPC25, NCAPH, NCAPH2, BUB1, FBXO5, SKA1, PPP3CA, ZWILCH, LFNG, CAMK2A, HELLS, ERCC91, EXO1, BOD1, MNM2, AK1, BIRC5, SIRT7, RACGAP1, SMC2, BRCAL, RGS14, SMCA, NOTCH2, CDKN1A, CCNB2, PHGDH, KIF20B, GAS2L1	1594	393	13588	1.69	1.18E-02	2.57E-04	5.99E-03
GOTERM_BP_FAT	GO:0022403-cell cycle phase	65	3.02	2.50E-05	KIFC1, E2F6, DBF4, PTTG1, FOXO4, CDC48, INCENP, ATF6B, TUBB8, CDCA2, RANBP1, CDCA3, CDC6, ARHGDF2, CCNK, KIF11, SGO2, SKP2, NUSAP1, GPR132, PLK1S1, MYH9, UBE2C, TACC3, HMG2A, UBE2B, CDK2, RBBP9, CCND1, MAD2L1, RCC2, ZWINT, BUB1B, STMN1, GADD45A, PP2R3A, NEK2, CAMK2G, POLA1, CHEK1, ANLN, CCNG1, SPC25, NCAPH, NCAPH2, BUB1, FBXO5, SKA1, PPP3CA, ZWILCH, LFNG, CAMK2A, HELLS, ERCC91, EXO1, BOD1, MNM2, AK1, BIRC5, SIRT7, RACGAP1, SMC2, BRCAL, RGS14, SMCA, NOTCH2, CDKN1A, CCNB2, PHGDH, KIF20B, GAS2L1	1594	328	13588	1.69	8.68E-02	1.49E-03	4.59E-02
Annotation Cluster 15 Category	Enrichment Score: 4.173406916287205	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
GOTERM_MF_FAT	GO:0030246-carbohydrate binding	64	2.98	7.74E-06	CD209A, POSTN, FSTL1, GPCPD1, CANX, SERPINE2, CD93, CD44, APOE, CLEC4A1, CLEC4A2, CLEC4D, CLEC4A3, MAN2B1, BSG, PCK1, MGP, CLEC4N, VEGFB, MAN2A2, SIGLEC1, MAN2A1, EGFAM, BGN, CLEC12A, NAV2, CD33, VEGFA, VCAM, LAMC2, CLEC4A, SLC6A1, GALT7, HSD17B12, CCL8, PA, CALR, CLEC1D, CCL7, ITGAM, HMMR, SMOCK2, PTX3, THBS1, GPNMB, SERPINF1, AGL, FN1, MRC1, LPL, PTPNRC, LMNAN1, LGALS3, SELL, LGALS1, FPM2A, FBNI, CHIL3, STAB2, LGALS9, LYVE1, STAB1, LAYN, CLEC7A, HSD17B12, CCL8, POSTN, PFA, FSTL1, CCL7, ITGAM, HMMR, SMOCK2, CD44, SERPINE2, APOE, GPNMB, THBS1, PTX3, AGL, FN1, LPL, PTPRC, FBNI, CHIL3, STAB2, VEGFB, LYVE1, BGN, EGFAM, STAB1, LAYN, NAV2, VEGFA, LAMC2, VCAM, CLEC7A	1524	317	13288	1.76	9.89E-03	5.52E-04	1.26E-02
GOTERM_MF_FAT	GO:0001871-pattern binding	33	1.53	1.39E-05	HSD17B12, CCL8, POSTN, PFA, FSTL1, CCL7, ITGAM, HMMR, SMOCK2, CD44, SERPINE2, APOE, GPNMB, THBS1, PTX3, AGL, FN1, LPL, PTPRC, FBNI, CHIL3, STAB2, VEGFB, LYVE1, BGN, EGFAM, STAB1, LAYN, NAV2, VEGFA, LAMC2, VCAM, CLEC7A	1524	128	13288	2.25	1.76E-02	8.47E-04	2.26E-02
GOTERM_MF_FAT	GO:0030247-polyaccharide binding	33	1.53	1.39E-05	NAV2, VEGFA, LAMC2, VCAM, CLEC7A	1524	128	13288	2.25	1.76E-02	8.47E-04	2.26E-02
Annotation Cluster 16 Category	Enrichment Score: 3.9596571907277394	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0007264-sGTPase mediated signal transduction	58	2.70	1.40E-06	GNA13, RAB5C, RASGEF1B, RRAD, RHOD, IQGAP2, RHOD, RGL1, IQGAP1, RAB2B, HMOX1, ARHGAP1, RHOA, RAB, RHOC, RHOG, RHOD, RAP2B, DBNL, RAP2A, BAA2P, RAB4B, GEM, ARHGEP1, ARL3, ELMO1, DNAAF27, DOK1, RHO, DOK2, DOK3, HRAS, BRAD, SDCBP, RAB12, ARAC, 5430435522RHK, ARF6, RAB44, RAB43, RAC2, RASGRP3, SOS2, ARHGSDA, RAB8A, RAB8B, VAV3, NRAS, RAB32, RAB11, ULK1, ARF1, ARF4, RAB34, VYHGA0, RHOT2, RAP1B, RAC3	1594	258	13588	1.92	5.09E-03	1.50E-04	2.58E-03
Annotation Cluster 17 Category	Enrichment Score: 3.651934493413683	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	
GOTERM_BP_FAT	GO:0043068-positive regulation of programmed cell death	56	2.60	2.45E-06	PDIA3, IL18, MMP9, BINP3, IL10, TGFBI, GPX1, CASP8, CASP3, CASP4, CASP9, BAX, APO1, HMOX1, NGFRAP1, NDUFS3, CASP1, MYC, PRKCA, CYCS, SKP2, NDUFA13, PRKCD, JMY, UNC13D, RPK3, BID, CDK5R1, LST1, ADAMTSL4, STK17B, SP110, BCL2L1, ALDH1A1, SHSAS, PYCARD, BCL3, NRP5D, DYRK2, TRP53, COL18A1, PTPN6, PTPN6, KLF13, NNAAL, FCGRI, BRCAL, FCGRI3, TRADD, NOTCH2, CDKN1A, UACA, BAX, ID3, APAF1, IFI204	1594	250	13588	1.91	8.88E-03	2.18E-04	4.51E-03
GOTERM_BP_FAT	GO:0010942-positive regulation of cell death	56	2.60	3.17E-06	PDIA3, IL18, MMP9, BINP3, IL10, TGFBI, GPX1, CASP8, CASP3, CASP4, CASP9, BAX, APO1, HMOX1, NGFRAP1, NDUFS3, CASP1, MYC, PRKCA, CYCS, SKP2, NDUFA13, PRKCD, JMY, UNC13D, RPK3, BID, CDK5R1, LST1, ADAMTSL4, STK17B, SP110, BCL2L1, ALDH1A1, SHSAS, PYCARD, BCL3, NRP5D, DYRK2, TRP53, COL18A1, PTPN6, PTPN6, KLF13, NNAAL, FCGRI, BRCAL, FCGRI3, TRADD, NOTCH2, CDKN1A, UACA, BAX, ID3, APAF1, IFI204	1594	252	13588	1.89	1.15E-02	2.56E-04	5.83E-03
GOTERM_BP_FAT	GO:0043065-positive regulation of apoptosis	55	2.56	4.18E-06	PDIA3, IL18, MMP9, BINP3, IL10, TGFBI, GPX1, CASP8, CASP3, CASP4, CASP9, BAX, APO1, HMOX1, NGFRAP1, NDUFS3, CASP1, MYC, PRKCA, CYCS, SKP2, NDUFA13, PRKCD, JMY, UNC13D, RPK3, BID, CDK5R1, LST1, ADAMTSL4, STK17B, SP110, BCL2L1, ALDH1A1, SHSAS, PYCARD, BCL3, NRP5D, DYRK2, TRP53, COL18A1, PTPN6, PTPN6, KLF13, NNAAL, FCGRI, BRCAL, FCGRI3, TRADD, NOTCH2, UACA, BAX, ID3, APAF1, IFI204	1594	248	13588	1.89	1.51E-02	3.24E-04	7.69E-03
Annotation Cluster 18 Category	Enrichment Score: 3.38309879598096	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR	

						PP1PSK2, PGAM1, PTPN22, PGAM2, PPP5K1, NTSC, PTPN1, PPAF2C, BFP2, PPP1R3A, LPIN2, PTPRO, LPIN3, PPM1H, PPM1L, PPM1M, PPF053, WTSC1A, RB30033F20R6, PPF051, PPM1A, ACPS, PTP1B, PPP3C8, PPP3CA, NPP5D, PPTC7, PTPN7, PTPN6, PTPN6C, PTPN6, PTPN18, PTPN3, PTPN4, PTPN4A, EPM2A, EPHK2, DUSP23, ATP1A1, BPOM, PTPN12, DUSP5, DUSP4, DUSP28, PTFPA3, DUSP26, PTPN1, PPTP1, DUSP8, DUSP6							
GOTERM_MF_FAT	GO:0016791~phosphatase activity	50	2.32	2.99E-05	PHPT1, DUSP8, DUSP6	1524	238	13288	1.83	3.77E-02	1.54E-03	4.88E-02	
Annotation Cluster 19 Category	Enrichment Score: 3.3671298805420657 Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
				MYO1A, PRKAG3, SLC73A1, PPARA, ACQYL, ACAD9B, ECH1, CPT2, STAT5B, NDUFB1, ECH1, CD74, HADHA, HADHB, SC4MDL, FAB1, ELOVL1, PRKAR2B, TNFRSF1A, ALOX5AP, PRKAA2, ELOVL6, HADH, HPGDS, GHR, ACSL5, SCD1, CPT1B, ACAA2, SCD2, ACADM, TRXAS1, NCF1, ALDH5A1, ACADS, PDPR, FADS1, PRKAR2, EPHK2, FADS3, CROT, PTHY, CPT1A, BRCA1, ACADVL, ALOX5, AACS, DEGS1	1594	184	13588	2.22	5.31E-04	2.12E-05	2.68E-04		
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	48	2.23	1.46E-07									
Annotation Cluster 25 Category	Enrichment Score: 2.4724967356094183 Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
				LST1, TNFRSF12A, PPT1, CALN, CDH4, TGFBI, DSTN, SLC11A1, ARPC2, RHOA, FCER1G, RANBP1, PTK3, SYNPO, TES, TRP53, PLEK, ACTA4, ULMK1, PLN2B, NUSAP1, CDK3, LDLRAP1, SRP9, FCGR1, FCGR3, FMN1, PLK4, FCGR2B, TPRP, CFL1, CLEC7A	1594	122	13588	2.24	7.30E-02	1.26E-03	3.83E-02		
GOTERM_BP_FAT	GO:0051130~positive regulation of cellular component organization	32	1.49	2.08E-05									
Annotation Cluster 27 Category	Enrichment Score: 2.4478334888926443 Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
				LIMA1, CAPZL1, ARPC5, VILL, DSTN, ACTR3, ARPC3, ARPC2, RHOA, RANBP1, SKA1, SYNPO, TES, DBNL, ARHGEF2, CCDC88A, PLEK, CEP192, MYO1F, TMSB10, MID1P1, FMN1, ARPC1B, PLK4, CORO1A, CFL1, CAPG, TMSB4X, STMN1	1594	99	13588	2.50	2.12E-02	4.29E-04	1.08E-02		
GOTERM_BP_FAT	GO:0051493~regulation of cytoskeleton organization	29	1.35	5.90E-06	DBNL, LIMA1, CCDC88A, PLEK, CAPZL1, MYO1F, TMSB10, ARPC5, VILL, DSTN, ACTR3, FMN1, ARPC1B, CORO1A, ARPC3, ARPC2, CFL1, CAPG, RHOA, TMSB4X, SYNPO	1594	60	13588	2.98	3.09E-02	6.04E-04	1.59E-02	
GOTERM_BP_FAT	GO:0032956~regulation of actin cytoskeleton organization	21	0.98	8.63E-06	DBNL, LIMA1, CCDC88A, PLEK, CAPZL1, MYO1F, TMSB10, ARPC5, VILL, DSTN, ACTR3, FMN1, ARPC1B, CORO1A, ARPC3, ARPC2, CFL1, CAPG, RHOA, TMSB4X, SYNPO	1594	61	13588	2.93	4.08E-02	7.56E-04	2.10E-02	
GOTERM_BP_FAT	GO:0032970~regulation of actin filament-based process	21	0.98	1.14E-05									
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	38	1.77	1.37E-05	LIMA1, LST1, CAPZL1, ARPC5, TGFBI, VILL, DSTN, ACTR3, CUL7, ARPC3, ARPC2, RHOA, RANBP1, SKA1, TES, SYNPO, TRP53, DBNL, ARHGEF2, CCDC88A, PLEK, CEP192, NUSAP1, MYO1F, TMSB10, HERC2, MID1P1, UBE2B, FMN1, ARPC1B, CORO1A, PLK4, YWHAH, MAD2L1, CFL1, CAPG, TMSB4X, STMN1	1594	154	13588	2.10	4.88E-02	8.77E-04	2.53E-02	
Annotation Cluster 30 Category	Enrichment Score: 2.3517354573541587 Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
				RASGEF1B, ARHGAP18, IQGAP2, ARHGAP15, RGL1, IQGAP1, TRC1D16, HMHA1, ARHGAP22, DMXL2, ARHGAP20, RINL, ARHGAP1, RANBP1, ARHGAP11A, DOCK10, DOCK11, DAR2IP, ARHGEF2, MAO2, ARHGEF6, RAB11L1, ARHGAP28, PSD4, ARHGEF9, ECT2, WAS, THY1, ARHGAP25, ARHGAP30, MAP4K4, RIN2, SRGAP3, RIN1, FGD2, ARFGAP3, TRC1D9, GIP5M3, CYTH4, MAP4K1, MYO9B, ADAP1, DOCK2, RASGRP3, GMP, SOS2, RASAL3, IQSEC3, RASA3, RAP1GAP2, FGD3, ARHGDIA, ARHGDIIB, OBSCN, TRC1D2B, VAV3, ABR, EXPH5, RGS18, DOCK8, RGS16, RACGAP1, DOCK5, VAV1, RGS14, ADAP2, RGS2, SH3BP1, ARAP1, BCAR3	1524	361	13288	1.69	1.45E-02	7.32E-04	1.86E-02		
GOTERM_MF_FAT	GO:0030693~GTPase regulator activity	70	3.25	1.14E-05	RASGEF1B, ARHGAP18, IQGAP2, ARHGAP15, RGL1, IQGAP1, TRC1D16, HMHA1, ARHGAP22, DMXL2, ARHGAP20, RINL, ARHGAP1, RANBP1, ARHGAP11A, DOCK10, DOCK11, DAR2IP, ARHGEF2, MAO2, ARHGEF6, RAB11L1, ARHGAP28, PSD4, ARHGEF9, ECT2, WAS, THY1, ARHGAP25, ARHGAP30, MAP4K4, RIN2, SRGAP3, RIN1, FGD2, ARFGAP3, TRC1D9, GIP5M3, CYTH4, MAP4K1, MYO9B, ADAP1, DOCK2, RASGRP3, GMP, SOS2, RASAL3, IQSEC3, RASA3, RAP1GAP2, FGD3, ARHGDIA, ARHGDIIB, OBSCN, TRC1D2B, VAV3, ABR, EXPH5, RGS18, DOCK8, RGS16, RACGAP1, DOCK5, VAV1, RGS14, ADAP2, RGS2, SH3BP1, ARAP1, BCAR3	1524	361	13288	1.69	1.45E-02	7.32E-04	1.86E-02	
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	70	3.25	2.01E-05	RASGEF1B, ARHGAP18, IQGAP2, ARHGAP15, RGL1, IQGAP1, TRC1D16, HMHA1, ARHGAP22, DMXL2, ARHGAP20, RINL, ARHGAP1, RANBP1, ARHGAP11A, DOCK10, DOCK11, DAR2IP, ARHGEF2, MAO2, ARHGEF6, RAB11L1, ARHGAP28, PSD4, ARHGEF9, ECT2, WAS, THY1, ARHGAP25, ARHGAP30, MAP4K4, RIN2, SRGAP3, RIN1, FGD2, ARFGAP3, TRC1D9, GIP5M3, CYTH4, MAP4K1, MYO9B, ADAP1, DOCK2, RASGRP3, GMP, SOS2, RASAL3, IQSEC3, RASA3, RAP1GAP2, FGD3, ARHGDIA, ARHGDIIB, OBSCN, TRC1D2B, VAV3, ABR, EXPH5, RGS18, DOCK8, RGS16, RACGAP1, DOCK5, VAV1, RGS14, ADAP2, RGS2, SH3BP1, ARAP1, BCAR3	1524	367	13288	1.66	2.55E-02	1.07E-03	3.27E-02	
Annotation Cluster 32 Category	Enrichment Score: 2.1864103669637593 Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
				IL18, STAT5B, HPS1, TLR2, PTPN22, TLR4, C1QC, PNP, TLR8, TGFBI, B2M, CFP, KLHL6, MYD88, HSP90AA1, LY86, NFKB1, CARD, THY1, C1QA, C1QB, LAT2, CD39, H2-AA, ITGAL, ILKRA, UNC93B1, IL7R, ADA, CD74, SLC11A1, FCER1G, IL2RG, SH2B2, NPP5D, THBS1, PTPN6, PTPN6C, CARD9, H2-M3, ICZF1, CFB, FCGR1, FCGR3, CORO1A, DCKN1A, PLCG2, CLEC7A, H2-DMA, SASH3	1594	206	13588	2.07	2.95E-03	8.94E-05	1.49E-03		
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	50	2.32	8.11E-07									
Annotation Cluster 58 Category	Enrichment Score: 1.561380646898854 Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
				ADCY7, ATP1B3, HPRT, ATP1B2, LQHD, PNP, MTHFD1L, ANK1, GOT1, HOC, IMPDH1, ATP5K, ATP8B4, HSP90AA1, FECH, ATP6V1H, PADI2, PADI4, ATP6V1A, NME1, AOK, RIN2, ATP5C1, ADSL, BCAT1, ALDH1B1, BCAT2, SRM, NAGS, ASNSD1, ASNS, AZIN1, CMPK1, ADA, TYMS, ATP6V0E, ALDH4A1, DCTD, TCIRG1, CEBA2, ODC1, ADSSL1, NOS1, NRP2, ATP1A1, ATP13A3, AMPD2, AMPD3, MMAB, ATP13A4, APRT, AMPD1, ADH1, P2RX4, ATP6V0E2, ADCY9, ATP2A2, SLC7A2, PHGDH, PSAT1, ATP8A1	1594	302	13588	1.72	8.85E-02	1.47E-03	4.68E-02		
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	61	2.84	2.55E-05									
Annotation Cluster 69 Category	Enrichment Score: 1.2861838620748725 Term	Count %	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
				BCAT1, BCKDHA, ALDH6A1, BCKDK, BCAT2, STAT5B, BCKDHB, HIBADH, GHR, AUH	1594	15	13588	5.68	3.77E-02	7.12E-04	1.94E-02		



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GOTERM_MF_FAT	GO:0032557-ribonucleotide binding	349	12.28	2.88E-06	ADOCY, GM6862, KFIC1, ADCY7, TUBB2B, TUBB2A, AUKR8, PKMG2, BTG, ACTG1, DDX11, RA828, OAS12, OAS1L, MAP3K8, MAP2K6, RAB27A, GBP8, PKIC3G, TYRO3, GBP5, SLCUG1, LIG1, MYH3, MYLK4, KIF5C, GBP9, MYLK2, IFI47, MYH7, WNK2, GEM, MYH9, RFC5, NME4, NME5, NAV1, RAB19, APCAP1, NEK8, PGDFRA, MAPK7, EIF2AK2, S43D4S5G22RHK, CHKA, GNA12, GNA2, NEK2, PFKF81, OAS3, UBA7, CHEK1, ARF6, MYO9B, OAS2, NAGK, EPHB8, EPHB2, VRK1, MOV10, RAC2, RAC3, POLQ, DDX58, SPHK1, TADK3, UBE2L6, ARC3, DDX4, RAD54L, ATP13A5, EPHA2, ABCG1, EPHA3, EPHA7, KCNB8, ARF3, ARF4, GRK4, RAD54B, GMA4951, CLCN5, NUAK2, MYO7A, ATPI0A, CAMKK1, CKB, CAMK2, ACTR3, ACTR2, NOD2, TUBB8, TUBB6, MASTL, DOCK10, AR1L5, SIK1, TOP2A, TARSL2, DDC7, COG6, LYN, PHKG1, NDUFA13, PKDC2, 170001780SRHK, BBS12, RAD51, MAST3, GM12250, PAPD4, ADK, RPK1, EIF4A1, ARL4C, RASD2, ARL4A, MYO5A, RAB18A, ALDH18A1, RAB10, CTNN4, HK1, NLRP1A, ITM2C, GCH1, IGF1R, GALX2, GALX1, RAB4A, RAB41, IGF7, PTX2B, CKMT2, HK3, BUB1, CERK, PAP51, PAP52, KF218, THRP13, ACSL5, MYO5C, ACTC1, SWAP70, POK3, ATP1A3, AXL, ATP14A, ACVY, PCZ2, RPS6KA6, RAB12, GMA548, RAB13, RPS6KA6, RPS6KA1, PYN, RAB3A, KIF3B, ABCC3, CHTF18, RAB38, GYK, CIT, DNMI1, KF20A, RNASEL, GNA15, PSTK, F13A1, PASK, RRAD, TTK, PMYMT1, PHA2B, MTHFD101, PKRAB28, AR1L3, NLR3, NLR3, RALB, MLK1, SAR1B, MX1, MX2, MATK, CITA, EGFR, POKK, MAP4K4, H2-OB, RPK3, OAS1B, OAS1C, UBA7, CHEK1, ARF6, MYO9B, OAS2, NAGK, EPHB8, EPHB2, VRK1, MOV10, RAC2, RAC3, POLQ, DDX58, SPHK1, FOXR2D2, TADK3, UBE2L6, ARCG2, DDX4, RAD54L, ATP13A5, EPHA2, ABCG1, EPHA3, EPHA7, KCNB8, ARF3, ARF4, GRK4, RAD54B, GMA4951, CLCN5, NUAK2, MYO7A, ATPI0A, CAMKK1, CKB, CAMK2, ACTR3, ACTR2, NOD2, TUBB8, TUBB6, MASTL, DOCK10, AR1L5, SIK1, TOP2A, TARSL2, DDC7, COG6, LYN, PHKG1, NDUFA13, PKDC2, 170001780SRHK, BBS12, RAD51, MAST3, GM12250, PAPD4, ADK, RPK1, EIF4A1, ARL4C, RASD2, ARL4A, MYO5A, RAB18A, ALDH18A1, RAB10, CTNN4, HK1, NLRP1A, ITM2C, GCH1, IGF1R, GALX2, GALX1, RAB4A, RAB41, IGF7, PTX2B, CKMT2, HK3, BUB1, CERK, PAP51, PAP52, KF218, THRP13, ACSL5, MYO5C, IRGM1, ACTC1, NDS1, SWAP70, POK3, ATP1A3, AXL, ATP14A, ACVY, PCZ2, RPS6KA6, RAB12, GMA548, RAB13, RPS6KA6, RPS6KA1, PYN, RAB3A, KIF3B, ABCC3, CHTF18, RAB38, GYK, CIT, DNMI1, RPS2A, RNASEL, GNA15, PSTK, F13A1, PASK, RRAD, TTK, PMYMT1, PHA2B, MTHFD101, PKRAB28, AR1L3, NLR3, NLR3, RALB, MLK1, SAR1B, MX1, MX2, MATK, CITA, EGFR, POKK, MAP4K4, H2-OB, RPK3, OAS1B, OAS1C, UBA7, CHEK1, ARF6, MYO9B, OAS2, NAGK, EPHB8, EPHB2, VRK1, MOV10, RAC2, RAC3, POLQ, DDX58, SPHK1, FOXR2D2, TADK3, UBE2L6, ARCG2, DDX4, RAD54L, ATP13A5, EPHA2, ABCG1, EPHA3, EPHA7, KCNB8, ARF3, ARF4, GRK4, RAD54B, GMA4951, CLCN5, NUAK2, MYO7A, ATPI0A, CAMKK1, CKB, CAMK2, ACTR3, ACTR2, NOD2, TUBB8, TUBB6, MASTL, DOCK10, AR1L5, SIK1, TOP2A, TARSL2, DDC7, COG6, LYN, PHKG1, NDUFA13, PKDC2, 170001780SRHK, BBS12, RAD51, MAST3, GM12250, PAPD4, ADK, RPK1, EIF4A1, ARL4C, RASD2, ARL4A, MYO5A, RAB18A, ALDH18A1, RAB10, CTNN4, HK1, NLRP1A, ITM2C, GCH1, IGF1R, GALX2, GALX1, RAB4A, RAB41, IGF7, PTX2B, CKMT2, HK3, BUB1, CERK, PAP51, PAP52, KF218, THRP13, ACSL5, MYO5C, IRGM1, ACTC1, NDS1, SWAP70, POK3, ATP1A3, AXL, ATP14A, ACVY, PCZ2, RPS6KA6, RAB12, GMA548, RAB13, RPS6KA6, RPS6KA1, PYN, RAB3A, KIF3B, ABCC3, CHTF18, RAB38, GYK, CIT, DNMI1, RPS2A, RNASEL, GNA15, PSTK, F13A1, PASK, RRAD, TTK, PMYMT1, PHA2B, MTHFD101, PKRAB28, AR1L3, NLR3, NLR3, RALB, MLK1, SAR1B, MX1, MX2, MATK, CITA, EGFR, POKK, MAP4K4, H2-OB, RPK3, OAS1B, OAS1C, UBA7, CHEK1, ARF6, MYO9B, OAS2, NAGK, EPHB8, EPHB2, VRK1, MOV10, RAC2, RAC3, POLQ, DDX58, SPHK1, FOXR2D2, TADK3, UBE2L6, ARCG2, DDX4, RAD54L, ATP13A5, EPHA2, ABCG1, EPHA3, EPHA7, KCNB8, ARF3, ARF4, GRK4, RAD54B, GMA4951, CLCN5, NUAK2, MYO7A, ATPI0A, CAMKK1, CKB, CAMK2, ACTR3, ACTR2, NOD2, TUBB8, TUBB6, MASTL, DOCK10, AR1L5, SIK1, TOP2A, TARSL2, DDC7, COG6, LYN, PHKG1, NDUFA13, PKDC2, 170001780SRHK, BBS12, RAD51, MAST3, GM12250, PAPD4, ADK, RPK1, EIF4A1, ARL4C, RASD2, ARL4A, MYO5A, RAB18A, ALDH18A1, RAB10, CTNN4, HK1, NLRP1A, ITM2C, GCH1, IGF1R, GALX2, GALX1, RAB4A, RAB41, IGF7, PTX2B, CKMT2, HK3, BUB1, CERK, PAP51, PAP52, KF218, THRP13, ACSL5, MYO5C, IRGM1, ACTC1, NDS1, SWAP70, POK3, ATP1A3, AXL, ATP14A, ACVY, PCZ2, RPS6KA6, RAB12, GMA548, RAB13, RPS6KA6, RPS6KA1, PYN, RAB3A, KIF3B, ABCC3, CHTF18, RAB38, GYK, CIT, DNMI1, RPS2A, RNASEL, GNA15, PSTK, F13A1, PASK, RRAD, TTK, PMYMT1, PHA2B, MTHFD101, PKRAB28, AR1L3, NLR3, NLR3, RALB, MLK1, SAR1B, MX1, MX2, MATK, CITA, EGFR, POKK, MAP4K4, H2-OB, RPK3, OAS1B, OAS1C, UBA7, CHEK1, ARF6, MYO9B, OAS2, NAGK, EPHB8, EPHB2, VRK1, MOV10, RAC2, RAC3, POLQ, DDX58, SPHK1, FOXR2D2, TADK3, UBE2L6, ARCG2, DDX4, RAD54L, ATP13A5, EPHA2, ABCG1, EPHA3, EPHA7, KCNB8, ARF3, ARF4, GRK4, RAD54B, GMA4951, CLCN5, NUAK2, MYO7A, ATPI0A, CAMKK1, CKB, CAMK2, ACTR3, ACTR2, NOD2, TUBB8, TUBB6, MASTL, DOCK10, AR1L5, SIK1, TOP2A, TARSL2, DDC7, COG6, LYN, PHKG1, NDUFA13, PKDC2, 170001780SRHK, BBS12, RAD51, MAST3, GM12250, PAPD4, ADK, RPK1, EIF4A1, ARL4C, RASD2, ARL4A, MYO5A, RAB18A, ALDH18A1, RAB10, CTNN4, HK1, NLRP1A, ITM2C, GCH1, IGF1R, GALX2, GALX1, RAB4A, RAB41, IGF7, PTX2B, CKMT2, HK3, BUB1, CERK, PAP51, PAP52, KF218, THRP13, ACSL5, MYO5C, IRGM1, ACTC1, NDS1, SWAP70, POK3, ATP1A3, AXL, ATP14A, ACVY, PCZ2, RPS6KA6, RAB12, GMA548, RAB13, RPS6KA6, RPS6KA1, PYN, RAB3A, KIF3B, ABCC3, CHTF18, RAB38, GYK, CIT, DNMI1, RPS2A, RNASEL, GNA15, PSTK, F13A1, PASK, RRAD, TTK, PMYMT1, PHA2B, MTHFD101, PKRAB28, AR1L3, NLR3, NLR3, RALB, MLK1, SAR1B, MX1, MX2, MATK, CITA, EGFR, POKK, MAP4K4, H2-OB, RPK3, OAS1B, OAS1C, UBA7, CHEK1, ARF6, MYO9B, OAS2, NAGK, EPHB8, EPHB2, VRK1, MOV10, RAC2, RAC3, POLQ, DDX58, SPHK1, FOXR2D2, TADK3, UBE2L6, ARCG2, DDX4, RAD54L, ATP13A5, EPHA2, ABCG1, EPHA3, EPHA7, KCNB8, ARF3, ARF4, GRK4, RAD54B, GMA4951, CLCN5, NUAK2, MYO7A, ATPI0A, CAMKK1, CKB, CAMK2, ACTR3, ACTR2, NOD2, TUBB8, TUBB6, MASTL, DOCK10, AR1L5, SIK1, TOP2A, TARSL2, DDC7, COG6, LYN, PHKG1, NDUFA13, PKDC2, 170001780SRHK, BBS12, RAD51, MAST3, GM12250, PAPD4, ADK, RPK1, EIF4A1, ARL4C, RASD2, ARL4A, MYO5A, RAB18A, ALDH18A1, RAB10, CTNN4, HK1, NLRP1A, ITM2C, GCH1, IGF1R, GALX2, GALX1, RAB4A, RAB41, IGF7, PTX2B, CKMT2, HK3, BUB1, CERK, PAP51, PAP52, KF218, THRP13, ACSL5, MYO5C, IRGM1, ACTC1, NDS1, SWAP70, POK3, ATP1A3, AXL, ATP14A, ACVY, PCZ2, RPS6KA6, RAB12, GMA548, RAB13, RPS6KA6, RPS6
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GOTERM_MF_FAT	GO:0030554=adenyl nucleotide binding	280	9.85	7.97E-06					1916	1535	13288	1.27	1.05E-02	4.22E-04	1.30E-02
ADOCY, KIFC1, ADCY7, AUKR8, PRKG2, BTK, ACTG1, DOK11, OASL2, OASL1, MAP3K8, MAP2N6, PKC3G, TYRO3, LUG1, MYH3, MYLK4, KIF5C, MYLK2, MYH7, WNK2, MYH9, RFXC, NME4, NMES, NAV1, ACAP1, DLD, NEKR, PDGFRA, MAPK7, EF2AK2, CHA4, NEK2, PFKFB1, OAS1, UBR47, CHEK1, MYO9B, OAS2, NAGK, EPHB3, EPHB2, VRK1, MOV10, POLQ, DHX58, SPHK1, FOXRED2, TADK3, UBE126, ABCG3, CDK4, RAD54L, ATP13A5, EPHA2, ABCG1, EPHA3, EPHA7, KCNIB, GRK4, RAD54B, CLCN5, NUAK2, MYO7A, ATP10A, CAMKK1, CAMK2K, CKB, ACTR3, ACT2, NOD2, MASTL, SIK1, TOP2A, TARSL2, CDCT, CDCE, LYN, PHG13, NDUFA13, PKDC, BBS1, RAD51, MAST3, PAP0A, SOLE, ADK, RPK1, EHF41, STEAP2, STEAP1, MYO5A, ALDH18A1, CETN4, HK1, NLRP1A, ITM2C, IGSF10, GALX2, GALX1, PTXZ8, CKMT2, HK3, BUB1, CERK, PAP51, PAP52, KIF218, TRIP13, ACSL5, MYO5C, ACTC1, NOS1, SWAP70, POK3, ATP1A3, AXL, ATP1A4, ACVY, RPS6KA4, RPS6KA4, RPS6KA1, FYN, KIF20B, ABCG3, CHTF18, GYK, CT, KIF20A, RNASEL, PSTK, F13A1, PASK, TTK, PPM1T1, PHAK2B, MTHFD1L, PRKAR2B, NLRCA, NLRX3, MLKL, MATK, EGRF, CITA, PDKX, MAP4K4, H2-OB, RPK3, OAS18, OAS1C, OAS1A, LRK1, OAS1G, PRPS2, XDH, IFH1, FGFFR4, ABCA9, FGR, ASS1, ACTR3B, STK10, PTYK, MAP4K1, CTP52, TIMPA, ABCA1, SRC, CMPK2, IRAK4, IRAK3, INP1, ENTDP1, RUNK1, RUNK2, HELLS, RUNK3, CSF3R, ERCC6G, TEC, AK1, MYO10, ATAD2, BRP1, MYO11F, ATAD5, PSMB8, PSMB9, DDX58, IKKBE, PXR4, DNAG2, P2RX7, PAK4, P2RX6, PLK3, PLK2, PLK1, MERTK, PIP4K2A, KIF23, KIF22, KIF24, SIFN9, PRPS2D, SIFN8, SIFN5, FES, SIFN1, SIFN4, ACSF2, SIFN1, SIFN2, TOR3A, KIF2C, MCM7, ATPB81, RHOB, ATPB82, MKK5, CSK, SUCLA2, CDK15, CDK14, ATPB8A, KIF14, CDK1, ACADM, KIF11, PKFL, LMCK1, KIF15, PPPK, CDK6, PRKM, PKM, CMCM1, UBE12C, PRKC, MCM4, UBE2B, CDK2, MCM5, DAPK1, PRKC8, MCM6, TOR2A, ATP10A, LCK, BUB1B, H2-AA, MELK, CAMK1D, FRK, DCK, ASK5, KIF9, NAIP6, NAIIP2, TAP2, KIF4, TAP1, DCLK1, CHD3, ACTB, ALPK1, FITK, HCK, KIF18B, CENPF, SMG2, GSG2, SMCA, CYBB, GCK, TPL1, APAF1, JAK3, H2-DMA, CDK20															
GOTERM_MF_FAT	GO:0001883=purine nucleoside binding	282	9.92	8.17E-06					1916	1548	13288	1.26	1.08E-02	4.16E-04	1.34E-02
ADOCY, KIFC1, ADCY7, AUKR8, PRKG2, BTK, ACTG1, DOK11, OASL2, OASL1, MAP3K8, MAP2N6, PKC3G, TYRO3, LUG1, MYH3, MYLK4, KIF5C, MYLK2, MYH7, WNK2, MYH9, RFXC, NME4, NMES, NAV1, ACAP1, DLD, NEKR, PDGFRA, MAPK7, EF2AK2, CHA4, NEK2, PFKFB1, OAS1, UBR47, CHEK1, MYO9B, OAS2, NAGK, EPHB3, EPHB2, VRK1, MOV10, POLQ, DHX58, SPHK1, FOXRED2, TADK3, UBE126, ABCG3, CDK4, RAD54L, ATP13A5, EPHA2, ABCG1, EPHA3, EPHA7, KCNIB, GRK4, RAD54B, CLCN5, NUAK2, MYO7A, ATP10A, CAMKK1, CAMK2K, CKB, ACTR3, ACT2, NOD2, MASTL, SIK1, TOP2A, TARSL2, CDCT, CDCE, LYN, PHG13, NDUFA13, PKDC, BBS1, RAD51, MAST3, PAP0A, SOLE, ADK, RPK1, EHF41, STEAP2, STEAP1, MYO5A, ALDH18A1, CETN4, HK1, NLRP1A, ITM2C, IGSF10, GALX2, GALX1, PTXZ8, CKMT2, HK3, BUB1, CERK, PAP51, PAP52, KIF218, TRIP13, ACSL5, MYO5C, ACTC1, NOS1, SWAP70, POK3, ATP1A3, AXL, ATP1A4, ACVY, RPS6KA4, RPS6KA4, RPS6KA1, FYN, KIF20B, ABCG3, CHTF18, GYK, CT, KIF20A, RNASEL, PSTK, F13A1, PASK, TTK, PPM1T1, PHAK2B, MTHFD1L, PRKAR2B, NLRCA, NLRX3, MLKL, MATK, EGRF, CITA, PDKX, MAP4K4, H2-OB, RPK3, OAS18, OAS1C, OAS1A, LRK1, OAS1G, PRPS2, XDH, IFH1, FGFFR4, ABCA9, FGR, ASS1, ACTR3B, STK10, PTYK, MAP4K1, CTP52, TIMPA, ABCA1, SRC, CMPK2, IRAK4, IRAK3, INP1, ENTDP1, RUNK1, RUNK2, HELLS, RUNK3, CSF3R, ERCC6G, TEC, AK1, MYO10, ATAD2, BRP1, MYO11F, ATAD5, PSMB8, PSMB9, DDX58, IKKBE, PXR4, DNAG2, P2RX7, PAK4, P2RX6, PLK3, PLK2, PLK1, MERTK, PIP4K2A, KIF23, KIF22, KIF24, SIFN9, PRPS2D, SIFN8, SIFN5, FES, SIFN1, SIFN4, ACSF2, SIFN1, SIFN2, TOR3A, KIF2C, MCM7, ATPB81, RHOB, ATPB82, MKK5, CSK, SUCLA2, CDK15, CDK14, ATPB8A, KIF14, CDK1, ACADM, KIF11, PKFL, LMCK1, KIF15, PPPK, CDK6, PRKM, PKM, CMCM1, UBE12C, PRKC, MCM4, UBE2B, CDK2, MCM5, DAPK1, PRKC8, MCM6, TOR2A, ATP10A, LCK, BUB1B, H2-AA, MELK, CAMK1D, FRK, DCK, ASK5, KIF9, NAIP6, NAIIP2, TAP2, KIF4, TAP1, DCLK1, CHD3, ACTB, ALPK1, FITK, HCK, KIF18B, CENPF, SMG2, GSG2, SMCA, CYBB, GCK, TPL1, APAF1, JAK3, H2-DMA, CDK20															
GOTERM_MF_FAT	GO:0001882=nucleoside binding	283	9.96	1.00E-06					1916	1558	13288	1.26	1.32E-02	4.75E-04	1.64E-02
ADOCY, KIFC1, ADCY7, AUKR8, PRKG2, BTK, ACTG1, DOK11, OASL2, OASL1, MAP3K8, MAP2N6, PKC3G, TYRO3, LUG1, MYH3, MYLK4, KIF5C, MYLK2, MYH7, WNK2, MYH9, RFXC, NME4, NMES, NAV1, ACAP1, DLD, NEKR, PDGFRA, MAPK7, EF2AK2, CHA4, NEK2, PFKFB1, OAS1, UBR47, CHEK1, MYO9B, OAS2, NAGK, EPHB3, EPHB2, VRK1, MOV10, POLQ, DHX58, SPHK1, FOXRED2, TADK3, UBE126, ABCG3, CDK4, RAD54L, ATP13A5, EPHA2, ABCG1, EPHA3, EPHA7, KCNIB, GRK4, RAD54B, CLCN5, NUAK2, MYO7A, ATP10A, CAMKK1, CAMK2K, CKB, ACTR3, ACT2, NOD2, MASTL, SIK1, TOP2A, TARSL2, CDCT, CDCE, LYN, PHG13, NDUFA13, PKDC, BBS1, RAD51, MAST3, PAP0A, SOLE, ADK, RPK1, EHF41, STEAP2, STEAP1, MYO5A, ALDH18A1, CETN4, HK1, NLRP1A, ITM2C, IGSF10, GALX2, GALX1, PTXZ8, CKMT2, HK3, BUB1, CERK, PAP51, PAP52, KIF218, TRIP13, ACSL5, MYO5C, ACTC1, NOS1, SWAP70, POK3, ATP1A3, AXL, ATP1A4, ACVY, RPS6KA4, RPS6KA4, RPS6KA1, FYN, KIF20B, ABCG3, CHTF18, GYK, CT, KIF20A, RNASEL, PSTK, F13A1, PASK, TTK, PPM1T1, PHAK2B, MTHFD1L, PRKAR2B, NLRCA, NLRX3, MLKL, MATK, EGRF, CITA, PDKX, MAP4K4, H2-OB, RPK3, OAS18, OAS1C, OAS1A, LRK1, OAS1G, PRPS2, XDH, IFH1, FGFFR4, ABCA9, FGR, ASS1, ACTR3B, STK10, PTYK, MAP4K1, CTP52, TIMPA, ABCA1, SRC, CMPK2, IRAK4, IRAK3, INP1, ENTDP1, RUNK1, RUNK2, HELLS, RUNK3, CSF3R, ERCC6G, TEC, AK1, MYO10, ATAD2, BRP1, MYO11F, ATAD5, PSMB8, PSMB9, DDX58, IKKBE, PXR4, DNAG2, P2RX7, PAK4, P2RX6, PLK3, PLK2, PLK1, MERTK, PIP4K2A, KIF23, KIF22, KIF24, SIFN9, PRPS2D, SIFN8, SIFN5, FES, SIFN1, SIFN4, ACSF2, SIFN1, SIFN2, TOR3A, KIF2C, MCM7, ATPB81, RHOB, ATPB82, MKK5, CSK, SUCLA2, CDK15, CDK14, ATPB8A, KIF14, CDK1, ACADM, KIF11, PKFL, LMCK1, KIF15, PPPK, CDK6, PRKM, PKM, CMCM1, UBE12C, PRKC, MCM4, UBE2B, CDK2, MCM5, DAPK1, PRKC8, MCM6, TOR2A, ATP10A, LCK, BUB1B, H2-AA, MELK, CAMK1D, FRK, DCK, ASK5, KIF9, NAIP6, NAIIP2, TAP2, KIF4, TAP1, DCLK1, CHD3, ACTB, ALPK1, FITK, HCK, KIF18B, CENPF, SMG2, GSG2, SMCA, CYBB, GCK, TPL1, APAF1, JAK3, H2-DMA, CDK20															
Annotation Cluster 10															
Category	Enrichment Score: 6.70100395814563516	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR			
GOTERM_BP_FAT	GO:0006897=endocytosis	60	2.11	4.54E-09	CD209A, MSRL, LDIR, MYO7A, SYN12, SYN21, MEGF10, CD47, DAB2, APP, NCEAP2, LBP, CAP1, GHR, DBNL, CNA3, STXBP1, ARHGAP27, COLEC12, SRPA, LDIRAP1, ELMO1, ZDHHC15, UNC130, LRP12, RIN2, FBP1S, RIN1, STEAP2, ANKFT1, SHG1L1, RAB3A, CDC42E1, NOSTRIN, PPT1, ABCAL, SLC11A1, DOKC1, FCER1G, MRC1L, MICALL2, HCK, MRC2, STAB2, FCGR1, VAV1, FCGR3, CORDIC, FNBP1, P2RX7, LRPI, FCGR2B, RAB34, IRF8, IRF9, CLEC7A, MERTK, DNMI1, CLN5, VLDLR	2002	188	13588	2.17	1.84E-05	4.28E-07	8.45E-06			
GOTERM_BP_FAT	GO:0010324=membrane invagination	60	2.11	4.54E-09	CD209A, MSRL, LDIR, MYO7A, SYN12, SYN21, MEGF10, CD47, DAB2, APP, NCEAP2, LBP, CAP1, GHR, DBNL, CNA3, STXBP1, ARHGAP27, COLEC12, SRPA, LDIRAP1, ELMO1, ZDHHC15, UNC130, LRP12, RIN2, FBP1S, RIN1, STEAP2, ANKFT1, SHG1L1, RAB3A, CDC42E1, NOSTRIN, PPT1, ABCAL, SLC11A1, DOKC1, FCER1G, MRC1L, MICALL2, HCK, MRC2, STAB2, FCGR1, VAV1, FCGR3, CORDIC, FNBP1, P2RX7, LRPI, FCGR2B, RAB34, IRF8, IRF9, CLEC7A, MERTK, DNMI1, CLN5, VLDLR	2002	188	13588	2.17	1.84E-05	4.28E-07	8.45E-06			
GOTERM_BP_FAT	GO:0006909=phagocytosis	24	0.84	7.78E-08	HCK, MYO7A, CDC42E1, COLEC12, ABCAL, MEGF10, VAV1, SRPA, FCGR1, FCGR3, ELMO1, CORDIC, APP, CD44, APOE, CTGF, COMP, APOH, PTH, THBS1, GPMR8, THSD2, AGL, FN1, PTHRC, FN1L, CORDIC, CH1L3, STAB2, COL5A3, COL5A1, NCAM1, TNFAIP6, LVLE1, EGFARM, NGN, STAB1, LAVN, VCAN	2002	49	13588	3.32	3.16E-04	5.45E-06	1.45E-04			
Annotation Cluster 11															
Category	Enrichment Score: 6.369786736238554	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR			
GOTERM_BP_FAT	GO:0016044=membrane organization	74	2.60	1.18E-07	CD209A, LKAT17, SYSD2, POLYBP1, FSTL1, POSTN, PDCP1, OGN, NOD2, APP, MAN2B2, CD44, CD93, CLEC4E, APOE, CTGF, APOH, CLEC4A1, CLEC4A, CLEC4B, MAN2B1, NGN, CLEC4A, COLEC12, PTHM, CLEC4N, NCAM1, MAN2A1, SUGLEC1, TNFAIP6, EGFARM, NGN, CLEC12A, CD3A, LAMC2, CLEC4B1, VCAN, CLEC5A, SUGLEC, GALNT7, MAMDC2, ENPP1, GALNT6, CD248, FCNA, GALNT4, HSD17B12, KLK1L1, CLCL8, PFA, CAAR, CLEC10A, ITGAM, CCL7, HMHR, CD9, COMP, CD22, PTH, CLEC2E, GPMR8, THBS1, SELV1S, THSD2, GALNT2, AGL, CLEC1, FN1, KLRK1, MRC1, PTHRC, FN1L, CORDIC, CH1L3, STAB2, COL5A3, COL5A1, NCAM1, TNFAIP6, LVLE1, EGFARM, NGN, STAB1, LAVN, VCAN	2002	272	13588	1.85	4.79E-04	7.86E-06	2.20E-04			
Annotation Cluster 12															
Category	Enrichment Score: 5.982599763257034	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR			
GOTERM_MF_FAT	GO:0030246=carbohydrate binding	93	3.27	8.84E-12	CD209A, LKAT17, SYSD2, POLYBP1, FSTL1, POSTN, PDCP1, OGN, NOD2, APP, MAN2B2, CD44, CD93, CLEC4E, APOE, CTGF, APOH, CLEC4A1, CLEC4A, CLEC4B, MAN2B1, NGN, CLEC4A, COLEC12, PTHM, CLEC4N, NCAM1, MAN2A1, SUGLEC1, TNFAIP6, EGFARM, NGN, CLEC12A, CD3A, LAMC2, CLEC4B1, VCAN, CLEC5A, SUGLEC, GALNT7, MAMDC2, ENPP1, GALNT6, CD248, FCNA, GALNT4, HSD17B12, KLK1L1, CLCL8, PFA, CAAR, CLEC10A, ITGAM, CCL7, HMHR, CD9, COMP, CD22, PTH, CLEC2E, GPMR8, THBS1, SELV1S, THSD2, GALNT2, AGL, CLEC1, FN1, KLRK1, MRC1, PTHRC, FN1L, CORDIC, CH1L3, STAB2, COL5A3, COL5A1, NCAM1, TNFAIP6, LVLE1, EGFARM, NGN, STAB1, LAVN, VCAN	1916	317	13288	2.03	1.17E-08	1.17E-08	1.45E-08			
GOTERM_MF_FAT	GO:0030247=polysaccharide binding	42	1.48	3.02E-07	ENPP1, MAMDC2, SYSD2, HSD17B12, POLYBP1, CLCL8, POSTN, PFA, FSTL1, ITGAM, CCL7, HMHR, NOD2, APP, CD44, APOE, CTGF, COMP, APOH, PTH, THBS1, GPMR8, THSD2, AGL, FN1, PTHRC, FN1L, CORDIC, CH1L3, STAB2, COL5A3, COL5A1, NCAM1, TNFAIP6, LVLE1, EGFARM, NGN, STAB1, LAVN, VCAN	1916	128	13288	2.28	4.00E-04	2.86E-05	4.95E-04			
GOTERM_MF_FAT	GO:0001871=pattern binding	42	1.48	3.02E-07	ENPP1, MAMDC2, SYSD2, HSD17B12, POLYBP1, CLCL8, POSTN, PFA, FSTL1, ITGAM, CCL7, HMHR, NOD2, APP, CD44, APOE, CTGF, COMP, APOH, PTH, THBS1, GPMR8, THSD2, AGL, FN1, PTHRC, FN1L, CORDIC, CH1L3, STAB2, COL5A3, COL5A1, NCAM1, TNFAIP6, LVLE1, EGFARM, NGN, STAB1, LAVN, VCAN	1916	128	13288	2.28	4.00E-04	2.86E-05	4.95E-04			
GOTERM_MF_FAT	GO:0005535=glycosaminoglycan binding	36	1.27	6.38E-07	MAMDC2, HSD17B12, POLYBP1, CLCL8, POSTN, PFA, FSTL1, ITGAM, CCL7, HMHR, NOD2, APP, CD44, APOE, CTGF, COMP, APOH, PTH, THBS1, GPMR8, THSD2, AGL, FN1, PTHRC, FN1L, CORDIC, CH1L3, STAB2, COL5A3, COL5A1, NCAM1, TNFAIP6, LVLE1, EGFARM, NGN, STAB1, LAVN, VCAN	1916	114	13288	2.19	8.42E-03	3.67E-04	1.04E-02			
Annotation Cluster 12															
Category	Enrichment Score: 5.982599763257034	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR			
GOTERM_BP_FAT	GO:0002822=regulation of adaptive immune response based on somatic recombination of immune rec	33	1.16	2.21E-11	CD209A, LKAT17, SYSD2, POLYBP1, FSTL1, POSTN, PDCP1, OGN, NOD2, APP, MAN2B2, CD44, CD93, CLEC4E, APOE, CTGF, APOH, CLEC4A1, CLEC4A, CLEC4B, MAN2B1, NGN, CLEC4A, COLEC12, PTHM, CLEC4N, NCAM1, MAN2A1, SUGLEC1, TNFAIP6, EGFARM, NGN, CLEC12A, CD3A, LAMC2, CLEC4B1, VCAN, CLEC5A, SUGLEC, GALNT7, MAMDC2, ENPP1, GALNT6, CD248, FCNA, GALNT4, HSD17B12, KLK1L1, CLCL8, PFA, CAAR, CLEC10A, ITGAM, CCL7, HMHR, CD9, COMP, CD22, PTH, CLEC2E, GPMR8, THBS1, SELV1S, THSD2, GALNT2, AGL, CLEC1, FN1, KLRK1, MRC1, PTHRC, FN1L, CORDIC, CH1L3, STAB2, COL5A3, COL5A1, NCAM1, TNFAIP6, LVLE1, EGFARM, NGN, STAB1, LAVN, VCAN	2002	56	13588	4.00	8.98E-10	4.73E-11	4.12E-10			
GOTERM_BP_FAT	GO:0002819=regulation of adaptive immune response	33	1.16	2.21E-11	CD209A, LKAT17, SYSD2, POLYBP1, FSTL1, POSTN, PDCP1, OGN, NOD2, APP, MAN2B2, CD44, CD93, CLEC4E, APOE, CTGF, APOH, CLEC4A1, CLEC4A, CLEC4B, MAN2B1, NGN, CLEC4A, COLEC12, PTHM, CLEC4N, NCAM1, MAN2A1, SUGLEC1, TNFAIP6, EGFARM, NGN, CLEC12A, CD3A, LAMC2, CLEC4B1, VCAN, CLEC5A, SUGLEC, GALNT7, MAMDC2, ENPP1, GALNT6, CD248, FCNA, GALNT4, HSD17B12, KLK1L1, CLCL8, PFA, CAAR, CLEC10A, ITGAM, CCL7, HMHR, CD9, COMP, CD22, PTH, CLEC2E, GPMR8, THBS1, SELV1S, THSD2, GALNT2, AGL, CLEC1, FN1, KLRK1, MRC1, PTHRC, FN1L, CORDIC, CH1L3, STAB2, COL5A3, COL5A1, NCAM1, TNFAIP6, LVLE1, EGFARM, NGN, STAB1, LAVN, VCAN	2002	56	13588	4.00	8.98E-10	4.73E-11	4.12E-10			
GOTERM_BP_FAT	GO:0002697=regulation of immune effector process	42	1.48	9.22E-13	ENPP1, MAMDC2, SYSD2, HSD17B12, POLYBP1, CLCL8, POSTN, PFA, FSTL1, ITGAM, CCL7, HMHR, NOD2, APP, CD44, APOE, CTGF, COMP, APOH, PTH, THBS1, GPMR8, THSD2, AGL, FN1, PTHRC, FN1L, CORDIC, CH1L3, STAB2, COL5A3, COL5A1, NCAM1, TNFAIP6, LVLE1, EGFARM, NGN, STAB1, LAVN, VCAN	2002	88	13588	3.24	3.74E-09	1.87E-10	1.72E-09			
GOTERM_BP_FAT	GO:0002703=regulation of leukocyte mediated immunity	35	1.23	1.89E-11	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	70	13588	3.39	7.67E-08	2.84E-09	3.51E-08			
GOTERM_BP_FAT	GO:0002706=regulation of lymphocyte mediated immunity	32	1.13	2.63E-11	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	65	13588	3.34	1.07E-06	3.44E-08	4.89E-07			
GOTERM_BP_FAT	GO:0002824=positive regulation of adaptive immune response based on somatic recombination of imm	21	0.74	3.65E-09	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	34	13588	4.19	1.48E-05	3.61E-07	6.79E-06			
GOTERM_BP_FAT	GO:0002821=positive regulation of adaptive immune response	21	0.74	3.65E-09	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	34	13588	4.19	1.48E-05	3.61E-07	6.79E-06			
GOTERM_BP_FAT	GO:0001914=regulation of T cell mediated cytotoxicity	11	0.39	4.46E-08	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	18	13588	5.28	2.48E-04	4.52E-06	1.14E-04			
GOTERM_BP_FAT	GO:0002709=regulation of T cell mediated immunity	14	0.49	6.12E-08	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	46	13588	3.39	3.98E-04	6.63E-06	1.82E-04			
GOTERM_BP_FAT	GO:0002699=positive regulation of immune effector process	23	0.81	9.71E-08	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	9	13588	6.79	6.92E-03	7.55E-05	3.18E-03			
GOTERM_BP_FAT	GO:0001916=positive regulation of T cell mediated cytotoxicity	9	0.32	1.79E-08	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	40	13588	3.22	1.74E-02	1.81E-04	8.03E-03			
GOTERM_BP_FAT	GO:0002708=positive regulation of lymphocyte mediated immunity	19	0.67	4.31E-06	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	40	13588	3.22	1.74E-02	1.81E-04	8.03E-03			
GOTERM_BP_FAT	GO:0002705=positive regulation of leukocyte mediated immunity	19	0.67	4.31E-06	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	40	13588	3.22	1.74E-02	1.81E-04	8.03E-03			
GOTERM_BP_FAT	GO:0031341=regulation of cell killing	16	0.56	5.44E-06	ADORA2B, IL27RA, C3, KLK1L, TNFSF13, CD101, IL7R, PNP, TGFBI, B2M, NOD2, SH2D1B1, TAP2, HMOK1, PPR3C, FCER1G, LAG3, SPN, CD28, H2-K1, FCERIA, PTHRC, IL7R, H2-M3, CENPD, CD40, H2-Q7, FCGR1, FCGR3, P2RX7, FCGR2B, TNFSF13B, SASH3	2002	30	13588	3.62	2.19E-02	2.23E-04	1.01E-02			

GOTERM_BP_FAT	GO:0001910~regulation of leukocyte mediated cytotoxicity	16	0.56	5.44E-06	H2 K1, PTPRC, H2 M3, KKR1, IL7R, CD101, PNP, H2 Q7, B2M, P2RX7, SH2D1B1, TAP2, ULBP1, PPP3C1, KLRB1, LAG3	2002	30	13588	3.62	2.19E-02	2.23E-04	1.01E-02
GOTERM_BP_FAT	GO:0002711~positive regulation of T cell mediated immunity	10	0.35	1.30E-05	H2 K1, PTPRC, P2RX7, H2 M3, TAP2, CD101, H2 Q7, PNP, SASH3, B2M	2002	13	13588	5.22	5.15E-02	4.77E-04	2.43E-02
Annotation Cluster 13	Enrichment Score: 5.973027397229028											
Category	Term	Count	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	69	2.43	1.84E-07	PD0A3, MMP9, IL18, BNP19, PMAIP1, TGFB1, CASP8, GPX1, NLRCA, CASP3, CASP4, CASP9, APOE, BOK, HMOX1, TICAM1, POU4F1, NGRAP1, CASP1, NDUFS3, MYC, LTB, SPN, RAB27A, CYCS, SKP2, NDUFA13, GZMB, GAL, PRKCD, BCL2L11, DAPK1, UNC13D, LCK, RPK3, BID, CXCR1, LST1, TNF, NFKBID, PML, NLRP1A, SP110, SRC, GCH1, ALDH1A1, SHSAs, PICARD, BCL3, INPP5D, CD27, RUNX3, CD28, COL18A1, PTPRC, PTPN6, FCGR1, BRCA1, FCGR3, TRADD, NOTCH2, EPHA7, P2RX7, CCKN1A, BIRC3, ENDOG, APAF1, IFI204, BARD1	2002	250	13588	1.87	7.48E-04	1.15E-05	3.43E-04
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	69	2.43	2.55E-07	PD0A3, MMP9, IL18, BNP19, PMAIP1, TGFB1, CASP8, GPX1, NLRCA, CASP3, CASP4, CASP9, APOE, BOK, HMOX1, TICAM1, POU4F1, NGRAP1, CASP1, NDUFS3, MYC, LTB, SPN, RAB27A, CYCS, SKP2, NDUFA13, GZMB, GAL, PRKCD, BCL2L11, DAPK1, UNC13D, LCK, RPK3, BID, CXCR1, LST1, TNF, NFKBID, PML, NLRP1A, SP110, SRC, GCH1, ALDH1A1, SHSAs, PICARD, BCL3, INPP5D, CD27, RUNX3, CD28, COL18A1, PTPRC, PTPN6, FCGR1, BRCA1, FCGR3, TRADD, NOTCH2, EPHA7, P2RX7, BIRC3, ENDOG, APAF1, IFI204, BARD1	2002	252	13588	1.86	1.04E-03	1.48E-05	4.75E-04
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	68	2.39	2.98E-07	STIL, MMP9, IL18, PMAIP1, GDNF, PNP, TGFB1, NLRCA, CUL7, APOE, NGRAP1, SPN, RAB27A, PIK3CG, ACTN4, MAD0, SKP2, POLB, BCL2L11, NMES, HIF1A, UNC13D, CDS98, CXCR1, RPK3, NGF, TRAF1, IFIH1, CCK81, LST1, NFKBID, PPT1, SP110, SOX9, ADA, CD74, SRC, IRAK3, FCER1G, FAIM, BMF, HELLS, RUNX3, TRAF4, ANOPT4, SPPI, COL18A1, PTPN6, TCF7, CARD9, SPHK1, HGF, GAS1, FCGR1, BRCA1, FCGR3, TRADD, NOTCH2, EPHA7, BCL2A10, P2RX7, CCKN1A, BCL2A1A, BIRC3, PLCG2, PDIA3, NUAKE2, BINP3, GLI3, KCNIP3, CASP6, GPX1, PCGF2, NOD2, CASP3, CASP4, CASP9, BOK, HMOX1, CASP8, TICAM1, POU4F1, CASP1, NDUFS3, MYC, LTB, CLN3, CYCS, NDUFA13, GZMB, GAL, PRKCD, UBE2B, DAPK1, SMO, CARD11, CARD14, TNFSF13B, BTCL, LCK, CAMK1D, BID, TNFRSF22, TNF, PRND, PML, NLRP1A, NLRP1B, GCH1, ALDH1A1, SHSAs, PICARD, BCL3, INPP5D, CD27, CD28, PTPRC, IL2RB, IL6, CENPF, BIRC5, SNAI2, ENDOG, APAF1, BARD1, IFI204	2002	248	13588	1.86	1.21E-03	1.70E-05	5.54E-04
GOTERM_BP_FAT	GO:0010941~regulation of cell death	127	4.47	4.83E-07	STIL, MMP9, IL18, PMAIP1, GDNF, PNP, TGFB1, NLRCA, CUL7, APOE, NGRAP1, SPN, RAB27A, PIK3CG, ACTN4, MAD0, SKP2, POLB, BCL2L11, NMES, HIF1A, UNC13D, CDS98, CXCR1, RPK3, NGF, TRAF1, IFIH1, CCK81, LST1, NFKBID, PPT1, SP110, SOX9, ADA, CD74, SRC, IRAK3, FCER1G, FAIM, BMF, HELLS, RUNX3, TRAF4, ANOPT4, SPPI, COL18A1, PTPN6, TCF7, CARD9, SPHK1, HGF, GAS1, FCGR1, BRCA1, FCGR3, TRADD, NOTCH2, EPHA7, BCL2A10, P2RX7, CCKN1A, BCL2A1A, BIRC3, PDIA3, NUAKE2, BINP3, GLI3, KCNIP3, CASP6, GPX1, PCGF2, NOD2, CASP3, CASP4, CASP9, BOK, HMOX1, CASP8, TICAM1, POU4F1, CASP1, NDUFS3, MYC, LTB, CLN3, CYCS, NDUFA13, GZMB, GAL, PRKCD, UBE2B, DAPK1, SMO, CARD11, CARD14, TNFSF13B, BTCL, LCK, CAMK1D, TNFRSF22, BID, TNF, PRND, PML, NLRP1A, NLRP1B, GCH1, ALDH1A1, SHSAs, PICARD, BCL3, INPP5D, CD27, CD28, PTPRC, IL2RB, IL6, CENPF, BIRC5, SNAI2, ENDOG, APAF1, BARD1, IFI204	2002	563	13588	1.53	1.96E-03	2.48E-05	8.98E-04
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	125	4.40	5.35E-07	STIL, MMP9, IL18, PMAIP1, GDNF, PNP, TGFB1, NLRCA, CUL7, APOE, NGRAP1, SPN, RAB27A, PIK3CG, ACTN4, MAD0, SKP2, POLB, BCL2L11, NMES, HIF1A, UNC13D, CDS98, CXCR1, RPK3, NGF, TRAF1, IFIH1, CCK81, LST1, NFKBID, PPT1, SP110, SOX9, ADA, CD74, SRC, IRAK3, FCER1G, FAIM, BMF, HELLS, RUNX3, TRAF4, ANOPT4, SPPI, COL18A1, PTPN6, TCF7, CARD9, SPHK1, HGF, GAS1, FCGR1, BRCA1, FCGR3, TRADD, NOTCH2, EPHA7, BCL2A10, P2RX7, CCKN1A, BCL2A1A, BIRC3, PDIA3, NUAKE2, BINP3, GLI3, KCNIP3, CASP6, GPX1, PCGF2, NOD2, CASP3, CASP4, CASP9, BOK, HMOX1, CASP8, TICAM1, POU4F1, CASP1, NDUFS3, MYC, LTB, CLN3, CYCS, NDUFA13, GZMB, GAL, PRKCD, UBE2B, DAPK1, SMO, CARD11, CARD14, TNFSF13B, BTCL, LCK, CAMK1D, TNFRSF22, BID, TNF, PRND, PML, NLRP1A, NLRP1B, GCH1, ALDH1A1, SHSAs, PICARD, BCL3, INPP5D, CD27, CD28, PTPRC, IL2RB, IL6, CENPF, BIRC5, SNAI2, ENDOG, APAF1, BARD1, IFI204	2002	553	13588	1.53	2.17E-03	2.68E-05	9.96E-04
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	126	4.43	6.20E-07	STIL, MMP9, IL18, PMAIP1, GDNF, PNP, TGFB1, NLRCA, CUL7, APOE, NGRAP1, SPN, RAB27A, PIK3CG, ACTN4, MAD0, SKP2, POLB, BCL2L11, NMES, HIF1A, UNC13D, CDS98, CXCR1, RPK3, NGF, TRAF1, IFIH1, CCK81, LST1, NFKBID, PPT1, SP110, SOX9, ADA, CD74, SRC, IRAK3, FCER1G, FAIM, BMF, HELLS, RUNX3, TRAF4, ANOPT4, SPPI, COL18A1, PTPN6, TCF7, CARD9, SPHK1, HGF, GAS1, FCGR1, BRCA1, FCGR3, TRADD, NOTCH2, EPHA7, BCL2A10, P2RX7, CCKN1A, BCL2A1A, BIRC3, PDIA3, NUAKE2, BINP3, GLI3, KCNIP3, CASP6, GPX1, PCGF2, NOD2, CASP3, CASP4, CASP9, BOK, HMOX1, CASP8, TICAM1, POU4F1, CASP1, NDUFS3, MYC, LTB, CLN3, CYCS, NDUFA13, GZMB, GAL, PRKCD, UBE2B, DAPK1, SMO, CARD11, CARD14, TNFSF13B, BTCL, LCK, CAMK1D, TNFRSF22, BID, TNF, PRND, PML, NLRP1A, NLRP1B, GCH1, ALDH1A1, SHSAs, PICARD, BCL3, INPP5D, CD27, CD28, PTPRC, IL2RB, IL6, CENPF, BIRC5, SNAI2, ENDOG, APAF1, BARD1, IFI204	2002	560	13588	1.53	2.51E-03	3.07E-05	1.15E-03
Annotation Cluster 14	Enrichment Score: 5.779005193758813											
Category	Term	Count	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042330~taxis	45	1.58	5.52E-11	NRP2, CSAR1, PLXNA3, CCL3, CCL2, S100A8, IL16, CYS1TR1, CXCL5, CCR1, SL37A4, S100A9, CCL9, CCL8, CXCR2, ITGB2, PF4, FPR2, CCL5, CXCL12, CCL4, ITGAM, CCL7, CCL6, CCL22, DOCK2, RAC2, ROBO1, CX1F, CSF3R, IL18, FCER1G, LBP, CSAR1, FCGR3, CCL12, CORO1A, CD97, CXCL13, CXCL16, CXCR1, CMTM7, CMTM8, CMTM9, PTPN6	2002	109	13588	2.80	2.24E-07	7.73E-09	1.03E-07
GOTERM_BP_FAT	GO:0006933~chemotaxis	45	1.58	5.52E-11	CMTM3, CMTM6, PTPN6	2002	109	13588	2.80	2.24E-07	7.73E-09	1.03E-07
GOTERM_BP_FAT	GO:0030595~leukocyte chemotaxis	15	0.53	6.50E-06	CSAR1, IL16, CCR1, S100A9, SL37A4, ITGB2, PF4, ITGAM, FCGR3, CORO1A, CXCR1, FCER1G, IL18, CSF3R, LBP	2002	27	13588	3.77	2.60E-02	2.56E-04	1.21E-02
GOTERM_BP_FAT	GO:0060326~cell chemotaxis	15	0.53	6.50E-06	NRP2, PLXNA3, S100A8, IL16, HEXA, HEXB, UCHL1, S100A8, CXCR2, CXCL12, APP, ROBO1, CSF3R, IL18, LBP, SEPL1, CSAR1, CCR7, CXCR1, CSTR, RASO2, CHL1, PTPAR, MYO5A, CSAR1, CCL3, CCL2, CYS1TR1, CXCL5, CCR1, SL37A4, CCL8, CCL6, RPT1, PF4, ITGB2, FPR2, CCL5, CCL4, COL7, ITGAM, CCL6, CCL22, DOCK2, P2Y1B, RAC2, CX1F, FCER1G, APRAL, NTS, APTJAS3, NPY1R, PAR1, FCGR3, CCL12, CORO1A, EFSR, CXCL13, CXCL16, CMTM7, CMTM8, CMTM9	2002	27	13588	3.77	2.60E-02	2.56E-04	1.21E-02
GOTERM_BP_FAT	GO:0007626~locomotory behavior	62	2.18	7.42E-06	NRP2, PLXNA3, S100A8, IL16, HEXA, HEXB, UCHL1, S100A8, CXCR2, CXCL12, APP, ROBO1, CSF3R, IL18, LBP, SEPL1, CSAR1, CCR7, CXCR1, CSTR, RASO2, CHL1, PTPAR, MYO5A, CSAR1, CCL3, CCL2, CYS1TR1, CXCL5, CCR1, SL37A4, CCL8, CCL6, RPT1, PF4, ITGB2, FPR2, CCL5, CCL4, COL7, ITGAM, CCL6, CCL22, DOCK2, P2Y1B, RAC2, CX1F, FCER1G, APRAL, NTS, APTJAS3, NPY1R, PAR1, FCGR3, CCL12, CORO1A, EFSR, CXCL13, CXCL16, CMTM7, CMTM8, CMTM9	2002	239	13588	1.76	2.97E-02	2.81E-04	1.38E-02
Annotation Cluster 15	Enrichment Score: 5.46846968893073											
Category	Term	Count	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030029~actin filament-based process	54	1.90	1.26E-07	LMA1, NUAKE2, AIF1, S100A9, WASF2, ACTG1, TMSB1S81, CAP1, RHOG, FMNL1, DBNL, ARHGFE2, ACTN4, ACTN1, TMSB10, MYH9, SIRPA, WAS, FLNA, ELMO1, TNNT2, FMNL1, C11, TMSB4X, DBNL1, LCP1, MYO5A, TCFP, CNXN3, MYH2, AMPCA, MYO9B, CAIR, PFN2, E2R, RAC2, RAC3, FAT1, SH2B2, CNR2, WIPF1, WIF2, ACTC1, RACGAP1, GAST, CORO1C, EPB4-1L2, EPB4-1L3, CORO1A, EPB4-1L1, EFSR, ANTXR1, DIA2, DIA3	2002	176	13588	2.08	5.10E-04	8.09E-06	2.34E-04
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	51	1.79	2.28E-07	LMA1, NUAKE2, AIF1, S100A9, WASF2, ACTG1, TMSB1S81, CAP1, RHOG, FMNL1, DBNL, ARHGFE2, ACTN4, ACTN1, TMSB10, MYH9, SIRPA, WAS, FLNA, ELMO1, TNNT2, FMNL1, C11, TMSB4X, DBNL1, LCP1, TCFP, CNXN3, MYH2, AMPCA, CAIR, PFN2, E2R, RAC2, RAC3, FAT1, SH2B2, CNR2, WIPF1, WIF2, ACTC1, RACGAP1, GAST, EPB4-1L2, CORO1C, EPB4-1L3, CORO1A, EPB4-1L1, EFSR, ANTXR1, DIA2, DIA3	2002	165	13588	2.10	9.27E-04	1.36E-05	4.25E-04
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	79	2.78	6.03E-06	CEPZ2, LMA1, NUAKE2, AIF1, WASF2, S100A9, VILL, ACTG1, TURBS, TMSB1S81, CAP1, TURB1B, RHOG, FMNL1, DBNL, ARHGFE2, KF11, ACTN4, ACTN1, NUSAP1, TMSB10, ESP11, PLK1S1, MYH9, TACC3, WAS, SIRPA, UBE2B, FLNA, TACC1, THY1, ELMO1, FMNL1, TNNT2, NAV1, TPPP, C11, TMSB4X, STMN1, HAUS8, DBNL1, LCP1, MYH2, CNXN3, TCFP, AMPCA, CAIR, SPIC5, PFN2, DOCK2, E2R, RAC2, RAC3, FAT1, FMOX1, CNR2, SH2B2, TIES, WIF2, ACTC1, CYP19C, NUP2, SPBP2, CNRP, NDC80, BIRC3, RACGAP1, GAST, BIRC4, CORO1C, EPB4-1L2, EPB4-1L3, CORO1A, EPB4-1L1, EFSR, LASP1, ANTXR1, DIA2, DIA3	2002	326	13588	1.64	2.42E-02	2.40E-04	1.12E-02
Annotation Cluster 16	Enrichment Score: 5.420191379823401											
Category	Term	Count	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0016651~oxidoreductase activity, acting on NADH or NADPH	24	0.84	1.30E-07	CYBBA3, NDUFB3, NDUFA5, NDUFB4, NDUFA2, GMPR2, NCF2, NDUFB8, NCF1, NDUFA7, NDUFC2, NDUFA13, CBRA, GMPR1, ECIS1, NDUFAF1, POR, NDUFA12, NDUFS7, NDUFS4, NDUFS8, NDUFV2, DLD, NDUFS3	1916	51	13288	3.26	1.72E-04	1.72E-05	2.13E-04
GOTERM_MF_FAT	GO:0050136~NADH dehydrogenase (quinone) activity	14	0.49	5.84E-06	NDUFB3, NDUFB4, NDUFA2, NDUFB8, NDUFA7, NDUFC2, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS3, NDUFB4, NDUFA2, NDUFB8, NDUFA7, NDUFC2, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS4, NDUFV2, NDUFS8, NDUFS3	1916	24	13288	4.05	7.70E-03	3.51E-04	9.55E-03
GOTERM_MF_FAT	GO:0003954~NADH dehydrogenase activity	14	0.49	5.84E-06	NDUFB3, NDUFB4, NDUFA2, NDUFB8, NDUFA7, NDUFC2, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS3, NDUFB4, NDUFA2, NDUFB8, NDUFA7, NDUFC2, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS4, NDUFV2, NDUFS8, NDUFS3	1916	24	13288	4.05	7.70E-03	3.51E-04	9.55E-03
GOTERM_MF_FAT	GO:0008137~NADH dehydrogenase (ubiquinone) activity	14	0.49	5.84E-06	NDUFB3, NDUFB4, NDUFA2, NDUFB8, NDUFA7, NDUFC2, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS3, NDUFB4, NDUFA2, NDUFB8, NDUFA7, NDUFC2, NDUFA13, NDUFAF1, NDUFA12, NDUFS7, NDUFS4, NDUFV2, NDUFS8, NDUFS3	1916	24	13288	4.05	7.70E-03	3.51E-04	9.55E-03
Annotation Cluster 17	Enrichment Score: 5.342784405964592											
Category	Term	Count	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	67	2.36	4.84E-12	LYHA, GNPDA1, PHK8, G6PD, PGM1, PGM2, ACN9, PDH8, MAN2B2, UGT1A7C, UGT1A6B, PPP1R1A, MAN2B1, MYC, B3GALT1, PKX1, PHG1, PKP, CHST2, CMAH, PKM, PPP1R3A, FBP2, PGM2, MAN2A1, RENBP, PGM1, SERP1, MDH1, RBP4, TNF, PFKFB1, SL37A4, PHKA1, PNK3, HK1, NAGK, GAUK2, GAUK1, THY1, PPK1R1C, PPP1R3B, HK3, ENO2, ENO3, GALE, GMYT, AGL, ENO1, GPD2, ALDOA1T1, GPD1, GMD5, PDK3, BPGM, NPY1R, PKC2, MAN1C1, OPT1A, CSGALNACT1, AMDHD2, ATF3, PYGM, GCK, PYGL, FABP5, PYGB	2002	191	13588	2.38	1.97E-08	8.55E-10	9.01E-09
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	60	2.11	4.06E-11	LYHA, GNPDA1, PHK8, G6PD, PGM1, PGM2, ACN9, PDH8, MAN2B2, UGT1A7C, UGT1A6B, PPP1R1A, MAN2B1, MYC, B3GALT1, PKX1, PHG1, PKP, CHST2, CMAH, PKM, PPP1R3A, FBP2, PGM2, MAN2A1, RENBP, PGM1, SERP1, MDH1, RBP4, TNF, PFKFB1, SL37A4, PHKA1, PNK3, HK1, NAGK, GAUK2, GAUK1, THY1, PPK1R1C, PPP1R3B, HK3, ENO2, ENO3, GALE, GMYT, AGL, ENO1, GPD2, ALDOA1T1, GPD1, GMD5, PDK3, BPGM, NPY1R, PKC2, MAN1C1, OPT1A, ATF3, PYGM, GCK, PYGL, FABP5, PYGB	2002	169	13588	2.41	1.65E-07	5.89E-09	7.56E-08
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	48	1.69	1.60E-08	RBP4, LYHA, TNF, PHK8, PHKA1, SL37A4, PGM1, PGM2, ACN9, PDH8, MAN2B2, UGT1A7C, UGT1A6B, PPP1R1A, MAN2B1, MYC, B3GALT1, PKX1, PHG1, PKP, CHST2, CMAH, PKM, PPP1R3A, FBP2, PGM2, MAN2A1, RENBP, PGM1, SERP1, MDH1, RBP4, TNF, PFKFB1, SL37A4, PHKA1, PNK3, HK1, NAGK, GAUK2, GAUK1, THY1, PPK1R1C, PPP1R3B, HK3, ENO2, ENO3, GALE, GMYT, AGL, ENO1, GPD2, ALDOA1T1, GPD1, GMD5, PDK3, BPGM, NPY1R, PKC2, MAN1C1, OPT1A, CSGALNACT1, AMDHD2, ATF3, PYGM, GCK, PYGL, GPM1, FABP5, SERP1, MDH1, PYGB	2002	140	13588	2.33	6.50E-05	1.38E-06	2.98E-05
Annotation Cluster 18	Enrichment Score: 5.29498240508022											
Category	Term	Count	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	87	3.06	1.98E-21	IL27RA, IL18, HPS1, IL12, TNFSF14, PTPN22, IL14, TNFSF13, CD101, C1QC, PNP, TGFBI, TLR8, B2M, CYP, NOD2, C18B, MYD88, KLRK1, HXK1, TICAM1, IRAK1, LAG3, SPN, H2 Q7, ICOSL, IL1N, CHL, CHAD, NFAM1, THY1, C1QA, C1QB, CARD11, CDR3, CD37, LAT2, CDRB, TNFSF13B, ULBP1, LCK, H2-AA, ITGAL, ADORA2B, C3, IL4RA, UNC93B1, KLRK1, CACNB3OR1,							

[illegible]



		RNASEL, PASK, STYX, PKMYT1, TTK, PTPN22, RORC, AURKB, PRKG2, TGFBI, BTK, PRKAR2B, APP, UQCRI0, UQCRI1, MDRF, MAP3KB, MLK1, MAP26A, MATK, PTPN1, PKCCE, EGFR, TYRO3, MADO, MYLK4, MYLK2, WNK2, PTPRN, PTPRO, MAP4K4, ACAP1, SLIC7A2, DLD, NEK8, ATP5C1, PGDGRA, RPK3, MAPK7, EIF2AK2, LRRK1, FGFR4, FGR, GNAQ, NEK2, STK10, SSH3, PTK7, ACPS, MAP4K1, CHEK1, EPHB3, SRC, CD74, EPHB2, IRAK4, IRAK3, VRK1, PTPB, CFIR, TSC, PTPN7, GPD2, MOD1, FCER1A, PTPN6, GPD1, PTPN18, TADK1, HGF, EPHA2, EPHA3, HKK6, EPHA7, DUSP28, P2RX7, PLK4, PLK3, PLK2, PLK1, GRK4, MERTK, ATP5E, IMPA2, NUAK2, SYNI1, FES, CAMKK1, CAMK2, CCNE1, SH2D1B1, ATP5L, ATP5O, MASTL, CSK, SIK1, ATP4V02, CDK15, ATP5H, CDK14, ATP5K, ATP5I, CDC7, CDK1, LYN, PHKG1, LIMK1, NDUFC2, CDK6, PDCC, PRK, PRKCD, CDK2, DAPK1, PRKCB, MAST3, OSM, ATP6V1A, CND1, PPM1E, UQCRIH, RPK1, PPM1H, CFL1, LCK, PPM1X, BUB1B, PPM1L, PPM1M, MEK, UQCRI, CAMK1D, PRK, NDUFB8, PPM1, PPM1A, ATP5G1, KGF5G, GALK2, GALK1, STAT4, PTK2B, PPP3CB, BUB1, DCLK1, TES, TCIRG1, PTPRC, ALPK1, PTPRE, FLT3, PDK3, HCK, PTPRA, NDUFA7, AXL, ATP5F1, CDKN3, GSG2, CDC25B, DUSP5, CCNB1, RPS6KA6, DUSP4, RPS6KA4, GCK, PTP4A3, RPS6KA1, FYN, GYK, JAK3, DUSP9, CIT, CKR2B, DUSP6												
GOTERM_BP_FAT	GO:0006793*phosphorus metabolic process	175	6.16	5.82E-06	CDK20, DUSP6			2002	866	13588	1.37	2.33E-02	2.36E-04	1.08E-02
Annotation Cluster 35	Enrichment Score: 2.5545766691173992													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0033559*unsaturated fatty acid metabolic process	19	0.67	6.23E-07	FCER1A, TBXAS1, PTGS2, NCF1, POPN, PAD2A1, EPH2, LTC4S, CD74, GGT5, TNFRSF1A, PTGS, PTGES, ALOX5AP, ALOX5, HPD, RNPEP, HPDGS, MGS2	2002	36	13588	3.58	2.53E-03	3.05E-05	1.16E-03		
GOTERM_BP_FAT	GO:0006690*icosanoid metabolic process	17	0.60	7.22E-06	HPGD, RNPEP, HPDGS, MGS2	2002	34	13588	3.39	2.89E-02	2.76E-04	1.34E-02		
Annotation Cluster 40	Enrichment Score: 2.3291168681773002													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0050777*negative regulation of immune response	14	0.49	2.33E-05	PTPRC, PTPN6, IL27RA, IL7R, TGFBI, GPX1, IRAK3, SH2D1B1, FCGR2B, CD59B, PPP3CB, INPP5D, KLKB1B, SPN	2002	26	13588	3.65	9.02E-02	8.00E-04	4.33E-02		
Annotation Cluster 43	Enrichment Score: 2.1580019024363786													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0031341*regulation of cell killing	16	0.56	5.44E-06	H2-K1, PTPRC, H2-M3, KLRK1, IL7R, CD101, PNP, H2-Q7, B2M, P2RX7, SH2D1B1, TAP2, ULBP1, PPP3CB, KLRB1B, LAG3	2002	30	13588	3.62	2.19E-02	2.23E-04	1.01E-02		
GOTERM_BP_FAT	GO:0001910*regulation of leukocyte mediated cytotoxicity	16	0.56	5.44E-06	H2-K1, PTPRC, H2-M3, KLRK1, IL7R, CD101, PNP, H2-Q7, B2M, P2RX7, SH2D1B1, TAP2, ULBP1, PPP3CB, KLRB1B, LAG3	2002	30	13588	3.62	2.19E-02	2.23E-04	1.01E-02		
Annotation Cluster 44	Enrichment Score: 2.143499635516042													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_BP_FAT	GO:0032101*regulation of response to external stimulus	33	1.16	1.87E-05	SBN2, ADORA2B, IL16, C3, TLRA, CXCL12, ADA, GPX1, TNFRSF1A, CD47, NOD2, TNFRSF1B, ADAH, APOH, FCER1G, LBP, THBS1, SPN, CD28, ZFP36, FCER1A, SELP, CLN3, PLEK, CD276, ADGR, FCGR1, FCGR3, ANKRD3, CD59B, FCGR2B, NPY, FAIM2	2002	103	13588	2.17	7.33E-02	6.62E-04	3.49E-02		
Annotation Cluster 50	Enrichment Score: 2.0226420719661573													
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR		
GOTERM_MF_FAT	GO:0015077*monovalent inorganic cation transmembrane transporter activity	33	1.16	1.79E-07	SLC36A1, ATP5E, SLC36A1, COX7B, COX7C, ATP5G1, UQCIF51, COX5A, COX5B, UQCRIQ, UQCRI0, UQCRI1, COX6B1, ATP5I, ATP5O, COX6B2, ATP5V02, ATP5H, ATP5K, ATP5L, TCIRG1, COX7A2, COX8B, COX7A1, ATP5F1, ATP1A3, ATP1A4, COX6C, ATP6V1A, UQCRIH, COX6A2, ATP5C1, UQCRIH, SLC36A1, COX7B, COX7C, ATP5G1, UQCIF51, COX5A, COX5B, UQCRIQ, UQCRI0, UQCRI1, COX6B1, ATP5I, ATP5O, COX6B2, ATP5V02, ATP5A, ATP5K, ATP5L, TCIRG1, COX7A2, COX8B, COX7A1, ATP5F1, COX6C, ATP6V1A, UQCRIH, COX6A2, ATP5C1, UQCRIH	1916	87	13288	2.63	2.37E-04	1.97E-05	2.93E-04		
GOTERM_MF_FAT	GO:0015078*hydrogen ion transmembrane transporter activity	31	1.09	4.92E-07	COX7A1, ATP5F1, COX6C, ATP6V1A, UQCRIH, COX6A2, ATP5C1, UQCRIH	1916	82	13288	2.62	6.51E-04	4.07E-05	8.05E-04		

b6 SLF GO Terms upregulated 168 hours post injury											
Annotation Cluster 1	Enrichment Score: 14.556398086357477	Count	Pvalue	Genes	List Total	Pop Hts	Pop Total	Fold Enrichment	Benferroni	FDR	
Category	Term										
GOTERM_BP_FAT	GO:0006955"immune response	49	14.16	6.60E-23 LY86, TLR2, CD103, CIQC, TURJ, IL10, CYP, OASL2, AF251705, NCF1, C4B, H2-DMB1, C1QA, C1QB, IL18BP, CCR5, IL1RB3, CXCR3, IL18RA, CCR2, OAS1A, IL12B, OAS1G, CD300A8, CD300D, CCL2, LST1, CCL9, CCL8, OAS2, CCL7, SLIC11A1, GP49A, FCER1G, CD4, CD7, TLRI3, MYO1F, CD300C, FCGR1, CD180, CCL17, FCGR3, CCL12, CD300A, PLCG2, FCER1, CLEC7A, XCL1, CD14	249	471	13588	5.68	1.03E-19	1.03E-19	1.00E-19
GOTERM_BP_FAT	GO:0006952"defense response	37	10.69	5.48E-14 CCL2, IL10, LY86, TLR2, CCL8, ITGB2, CIQC, TURJ, CIQC, CCL7, IL10, CYP, SLIC11A1, PYCARD, FCER1G, LY22, C4B, NCF1, HCK, CAMP, TLRI3, SAA3, MYO1F, CDT11, FCGR1, CD180, FCGR3, CCL17, C1QA, C1QB, CCL12, CCR5, IFI8, CCR2, CLEC7A, CD14, ORMD2	249	448	13588	4.51	8.55E-11	4.28E-11	9.15E-11
GOTERM_BP_FAT	GO:0006954"inflammatory response	26	7.51	4.19E-13 CCL2, LY86, TLR2, CCL8, ITGB2, CIQC, TURJ, CCL7, CYP, SLIC11A1, PYCARD, NCF1, C4B, TLRI3, SAA3, FCGR1, CD180, FCGR3, C1QA, CCL12, C1QB, CCR5, CCR2, CLEC7A, ORMD2, CD14	249	225	13588	6.31	6.51E-10	2.18E-10	6.99E-10
GOTERM_BP_FAT	GO:0096117"response to wounding	29	8.38	3.92E-11 CCL2, LY86, TLR2, CCL8, ITGB2, CIQC, TURJ, CCL7, CYP, SLIC11A1, PYCARD, TTP2, PLEK, GATM, NCF1, C4B, TLRI3, SAA3, FCGR1, CD180, FCGR3, C1QA, C1QB, CCL12, CCR5, CCR2, CLEC7A, ORMD2, CD14	249	347	13588	4.56	6.12E-08	1.53E-08	6.55E-08
Annotation Cluster 2	Enrichment Score: 5.491123660575224	Count	Pvalue	Genes	List Total	Pop Hts	Pop Total	Fold Enrichment	Benferroni	FDR	
Category	Term										
GOTERM_BP_FAT	GO:0047242"defense response to bacterium	13	3.76	6.20E-07 LY22, FGR, NCF1, CAMP, HCK, TURJ, MYO1F, FCGR1, IL10, SLIC1A1, CCR5, IFI8, FCER1G	249	108	13588	6.57	9.66E-04	6.90E-05	1.03E-03
GOTERM_BP_FAT	GO:0096117"response to bacterium	15	4.34	1.08E-06 LY22, FGR, NCF1, CAMP, HCK, TURJ, MYO1F, FCGR1, IL10, SLIC1A1, CCR5, IFI8, PLCG2, FCER1G, CD14	249	157	13588	5.21	1.69E-03	1.13E-04	1.81E-03
Annotation Cluster 3	Enrichment Score: 4.990727463947588	Count	Pvalue	Genes	List Total	Pop Hts	Pop Total	Fold Enrichment	Benferroni	FDR	
Category	Term										
GOTERM_BP_FAT	GO:0001819"positive regulation of cytokine production	11	3.18	1.60E-07 CD83, SLIC1A1, KLR1, PYCARD, TLRI2, FCER1G, CLEC7A, CASP1, TURJ, SASH3, CD14	249	62	13588	9.68	2.49E-04	2.27E-05	2.67E-04
GOTERM_BP_FAT	GO:0001817"regulation of cytokine production	15	4.34	2.44E-07 TLRI2, FGR, NCF1, CAMP, HCK, TURJ, MYO1F, FCGR1, IL10, SLIC1A1, CCR5, IFI8, FCER1G, CLEC7A, CASP1, SASH3, CD14	249	139	13588	5.89	3.80E-04	3.16E-05	4.07E-04
Annotation Cluster 4	Enrichment Score: 4.97611947115325	Count	Pvalue	Genes	List Total	Pop Hts	Pop Total	Fold Enrichment	Benferroni	FDR	
Category	Term										
GOTERM_BP_FAT	GO:0042330"axis	15	4.34	1.08E-08 CXCR1, CCL2, CCL9, CCL8, ITGB2, CCL7, CCL17, FCGR3, CCL12, CD30A1, RAC2, CXCR3, FCER1G, XCR1, XCL1	249	109	13588	7.51	1.69E-05	1.88E-06	1.81E-05
GOTERM_BP_FAT	GO:0006935"chemotaxis	15	4.34	1.08E-08 CXCR1, CCL2, CCL9, CCL8, ITGB2, CCL7, CCL17, FCGR3, CCL12, CD30A1, RAC2, CXCR3, FCER1G, XCR1, XCL1	249	109	13588	7.51	1.69E-05	1.88E-06	1.81E-05
GOTERM_MF_FAT	GO:0008009"chemokine activity	7	2.02	2.84E-05 CCL12, CCL9, CCL8, XCL1, CCL7, CCL17	214	38	13288	11.44	9.14E-03	4.58E-03	3.84E-02
GOTERM_MF_FAT	GO:0042379"chemokine receptor binding	7	2.02	3.32E-05 CCL12, CCL1, CCL9, CCL8, XCL1, CCL7, CCL17	214	39	13288	11.14	1.07E-02	3.56E-03	4.48E-02
Annotation Cluster 5	Enrichment Score: 4.734364155773175	Count	Pvalue	Genes	List Total	Pop Hts	Pop Total	Fold Enrichment	Benferroni	FDR	
Category	Term										
GOTERM_BP_FAT	GO:0005775"cell activation	24	6.94	1.31E-10 FYE, LST1, PLEK, MYO1F, RORC, ITGB2, SFPI1, CD1D1, WAS, FCGR3, CD4B, SLIC2A1D, CD86, IL1RB3, PLCG2, CXCR3, KLR1, FCER1G, CD14, IL12B, HELLS, RHOM, LP2	249	246	13588	5.32	2.04E-07	4.08E-08	2.19E-07
GOTERM_BP_FAT	GO:0045321"leukocyte activation	22	6.36	5.46E-10 FYE, MYO1F, RORC, ITGB2, SFPI1, CD1D1, WAS, FCGR3, CD4B, SLIC2A1D, CD86, IL1RB3, PLCG2, CXCR3, KLR1, FCER1G, CD14, IL12B, HELLS, RHOM, LP2	249	219	13588	5.48	8.52E-07	1.42E-07	9.12E-07
GOTERM_BP_FAT	GO:0002274"myeloid leukocyte activation	10	2.89	9.07E-09 FYE, SLIC1A1, IL1RB3, CXCR3, MYO1F, FCER1G, SFPI1, LP2, RHOM, FCGR3	249	35	13588	15.59	1.41E-07	1.17E-07	1.51E-05
GOTERM_BP_FAT	GO:0046649"lymphocyte activation	15	4.34	1.09E-05 RHOH	249	191	13588	4.29	1.68E-02	8.46E-04	1.81E-02
Annotation Cluster 6	Enrichment Score: 4.102642801925643	Count	Pvalue	Genes	List Total	Pop Hts	Pop Total	Fold Enrichment	Benferroni	FDR	
Category	Term										
GOTERM_BP_FAT	GO:0005884"positive regulation of immune system process	21	6.07	1.15E-09 C4B, TLRI2, CD101, CIQC, FCGR1, FCGR3, CYP, C1QA, C1QB, SLIC1A1, CD8B, BCL2A1D, CD30A1, PLCG2, KLR1, FCER1G, CD14, IL2RG, IL2R, CLEC7A, SASH3	249	206	13588	5.56	1.79E-06	2.56E-07	1.92E-06
GOTERM_BP_FAT	GO:0050778"positive regulation of immune response	16	4.62	2.64E-08 C4B, TLRI2, CD101, CIQC, FCGR1, FCGR3, CYP, C1QA, C1QB, SLIC1A1, BCL2A1D, PLCG2, KLR1, FCER1G, CLEC7A, SASH3	249	136	13588	6.62	4.11E-05	4.11E-06	4.40E-05
GOTERM_BP_FAT	GO:0040807"innate immune response	13	3.76	5.60E-07 C4B, TLRI3, TLR2, CD101, CIQC, FCGR1, FCGR3, TURJ, CD30B, C1QA, CYP, SLIC1A1, C1QB, CLEC7A, C4B, TLRI2, CD101, CIQC, FCGR1, FCGR3, CYP, C1QA, C1QB, SLIC1A1, BCL2A1D, PLCG2, KLR1, FCER1G, CLEC7A, SASH3	249	107	13588	6.83	8.73E-04	6.72E-05	9.35E-04
GOTERM_BP_FAT	GO:0048584"positive regulation of response to stimulus	16	4.62	1.60E-06 C1QA, FCER1G, CLEC7A, SASH3	249	186	13588	4.69	2.50E-03	1.56E-04	2.68E-03
GOTERM_BP_FAT	GO:0002352"immune effector process	13	3.76	3.24E-06 NCF1, C4B, MYO1F, CIQC, FCGR1, TLRI7, FCGR3, C1QA, CYP, SLIC1A1, C1QB, IL1RB3, FCER1G	249	126	13588	5.63	5.04E-03	2.97E-04	5.41E-03
GOTERM_BP_FAT	GO:0002357"activation of immune response	11	3.18	3.59E-06 C1QA, CYP, BCL2A1D, CD14, IL2, KLR1, TURJ, FCER1G, CLEC7A, CIQC	249	86	13588	6.98	5.28E-03	2.15E-04	5.09E-03
GOTERM_BP_FAT	GO:0002443"leukocyte mediated immunity	11	3.18	4.91E-06 C1QA, C1QB, SLIC1A1, NCF1, C4B, IL1RB3, MYO1F, FCER1G, CIQC, FCGR1, FCGR3	249	89	13588	6.74	7.63E-03	4.03E-04	8.20E-03
GOTERM_BP_FAT	GO:0002250"adaptive immune response	10	2.89	2.17E-05 C1QA, C1QB, SLIC1A1, IL18BP, C4B, IL1RB3, FCER1G, CIQC, FCGR1, FCGR3	249	84	13588	6.50	3.33E-02	1.61E-03	3.63E-02
GOTERM_BP_FAT	GO:0002460"adaptive immune response based on somatic recombination of immune receptors but fr	10	2.89	2.17E-05 C1QA, C1QB, SLIC1A1, IL18BP, C4B, IL1RB3, FCER1G, CIQC, FCGR1, FCGR3	249	84	13588	6.50	3.33E-02	1.61E-03	3.63E-02
Annotation Cluster 7	Enrichment Score: 3.09628777308218895	Count	Pvalue	Genes	List Total	Pop Hts	Pop Total	Fold Enrichment	Benferroni	FDR	
Category	Term										
GOTERM_BP_FAT	GO:0050778"positive regulation of immune response	16	4.62	2.64E-08 FCER1G, CLEC7A, SASH3	249	136	13588	6.62	4.11E-05	4.11E-06	4.40E-05
GOTERM_BP_FAT	GO:0048584"positive regulation of response to stimulus	16	4.62	1.60E-06 C4B, TLRI2, CD101, CIQC, FCGR1, FCGR3, C1QA, CYP, C1QB, SLIC1A1, BCL2A1D, PLCG2, KLR1, FCER1G, CLEC7A, SASH3	249	186	13588	4.69	2.50E-03	1.56E-04	2.68E-03
Annotation Cluster 12	Enrichment Score: 2.1332794229095495	Count	Pvalue	Genes	List Total	Pop Hts	Pop Total	Fold Enrichment	Benferroni	FDR	
Category	Term										
GOTERM_BP_FAT	GO:0006909"phagocytosis	8	2.31	2.77E-05 SLIC1A1, HCK, IFI8, FCER1G, CLEC7A, MEGF10, FCGR1, FCGR3	249	49	13588	8.91	4.23E-02	1.96E-03	4.62E-02
Annotation Cluster 13	Enrichment Score: 2.048358806290177	Count	Pvalue	Genes	List Total	Pop Hts	Pop Total	Fold Enrichment	Benferroni	FDR	
Category	Term										
GOTERM_MF_FAT	GO:0019955"cytokine binding	11	3.18	1.38E-06 IL18BP, CCR5, CSF2R2, IL10, CCL2, CXCR3, CSF2RA, IL2RG, IL12B, XCR1, CSF2RA	214	88	13288	7.76	4.45E-04	4.45E-04	1.86E-04

Annotation Cluster 1      Enrichment Score: 14.556398086357477

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006955~immune response	49	14.16	6.60E-23	LY86, TUR2, CD101, C1QC, TUR1, IL10, CYP, DAS2, AF251705, NCF1, C4B, H2-DMB1, C1QA, C1QB, KLBP, CCR5, LUBB3, CXCR1, IL18RA, CCL7, GAS2A, IL12B, DAS16, CD200B, CD500B, C127, LIT1, CCL9, LUB3, CD29, CCL31A1, GPMR, FCER1G, CD4, C07, TUR13, MYO1F, CD300C, FCER1G, CD180, CCL18, OAS2, CCL12, CD300A, PLCG2, IFNRA, CLEC7A, XCL1, CD14	249	471	13588	5.68	1.03E-19	1.03E-19	1.10E-19
					C1QB, C1Q, LY86, TUR2, C4B, IFNRA, CD101, TUR1, C1QC, C1Q, IL10, CYP, CCL31A1, PYCARD, FCER1G, LY2Z, C4B, NCF1, HCK, CAMP, TUR13, SAA2, MYO1F, C071L, FCER1G, CD180, FCGR3, CCL17, C1QA, C1QB, CCL12, CCR5, IRF8, CCR2, CLEC7A, CD14, ORMD2	249	448	13588	4.51	8.55E-11	4.28E-11	9.15E-11
GOTERM_BP_FAT	GO:0006954~inflammatory response	26	7.51	4.19E-13	CCL2, LY86, TUR2, CCL8, ITGB2, C1QC, TUR1, C1Q, CYP, CCL31A1, PYCARD, NCF1, C4B, TUR13, SAA3, FCGR1, CD180, FCGR3, C1QA, CCL12, C1QB, CCR5, CCR2, CLEC7A, ORMD2, CD14	249	225	13588	6.31	6.53E-10	2.18E-10	6.99E-10
GOTERM_BP_FAT	GO:0096111~response to wounding	29	8.38	3.92E-11	CCL8, LY86, TUR2, CCL8, ITGB2, C1QC, TUR1, C1Q, CYP, CCL31A1, PYCARD, TPPI2, C1Q, GATM, NCF1, C4B, TUR13, SAA3, FCGR1, CD180, FCGR3, C1QA, C1QB, CCL12, CCR5, CCR2, CLEC7A, ORMD2, CD14	249	347	13588	4.56	6.12E-08	1.53E-08	6.55E-08
Annotation Cluster 2 Category	Enrichment Score: 5.491213660755224 Term	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Benferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042742~defense response to bacterium	13	3.76	6.20E-07	LY2Z, FGR, NCF1, CAMP, HCK, TUR2, MYO1F, FCGR1, IL10, CCL31A1, CCR5, IRF8, FCER1G	249	108	13588	6.57	9.66E-04	6.90E-05	1.03E-03
GOTERM_BP_FAT	GO:0006171~response to bacterium	15	4.34	1.08E-06	LY2Z, FGR, NCF1, CAMP, HCK, TUR2, MYO1F, FCGR1, IL10, CCL31A1, CCR5, IRF8, PLCG2, FCER1G, CD14	249	157	13588	5.21	1.69E-03	1.13E-04	1.81E-03
Annotation Cluster 3 Category	Enrichment Score: 4.990727463947588 Term	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Benferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001819~positive regulation of cytokine production	11	3.18	1.60E-07	CD83, CCL31A1, KLRE1, PYCARD, TUR2, FCER1G, CLEC7A, CASP1, TUR1, SASH3, CD14, TUR2, CD101, TUR17, IL10, FCGR3, CD83, HHMOX1, KLR1, PYCARD, FCER1G, CLEC7A, CASP1, SASH3, CD14	249	62	13588	9.68	2.49E-04	2.27E-05	2.67E-04
GOTERM_BP_FAT	GO:0001817~regulation of cytokine production	15	4.34	2.44E-07	TUR2, CD101, TUR17, IL10, FCGR3, CD83, HHMOX1, KLR1, PYCARD, FCER1G, CLEC7A, CASP1, SASH3, CD14	249	139	13588	5.89	3.80E-04	3.16E-05	4.07E-04
Annotation Cluster 4 Category	Enrichment Score: 4.97611947115325 Term	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Benferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042330~axis	15	4.34	1.08E-08	CSAR1, CCL2, CCL9, CCL8, ITGB2, CCL17, FCGR3, CCL12, CORO1A, RAC2, CXCR1, FCER1G, XCR1, CXAR1, CCL1, CCL9, CCL8, ITGB2, CCL17, FCGR3, CCL12, CORO1A, RAC2, CXCR1, FCER1G, XCR1, CCL1	249	109	13588	7.51	1.69E-05	1.88E-06	1.81E-05
GOTERM_BP_FAT	GO:0006935~chemotaxis	15	4.34	1.08E-08	XCL1	249	109	13588	7.51	1.69E-05	1.88E-06	1.81E-05
GOTERM_MF_FAT	GO:0008009~chemokine activity	7	2.02	2.84E-05	CCL12, CCL2, CCL9, CCL8, XCL1, C07, CCL17	214	38	13288	11.44	9.14E-03	4.58E-03	3.84E-02
GOTERM_MF_FAT	GO:0042379~chemokine receptor binding	7	2.02	3.32E-05	CCL12, CCL2, CCL9, CCL8, XCL1, C07, CCL17	214	39	12888	11.14	1.07E-02	3.56E-03	4.48E-02
Annotation Cluster 5 Category	Enrichment Score: 4.794364155737175 Term	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Benferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001775~cell activation	24	6.94	1.31E-10	FYB, LST1, PLEK, MYO1F, RORC, ITGB2, SFPI1, CD101, WAS, FCGR3, CD48, SLC11A1, BCL2A1D, CD86, IL18B3, PLCG2, CXCR1, KLR1, FCER1G, CD4, IL12B, HELLS, RHMO, LPD2	249	246	13588	5.32	2.04E-07	4.08E-08	2.19E-07
GOTERM_BP_FAT	GO:0045321~leukocyte activation	22	6.36	5.46E-10	PYB, MYO1F, RORC, ITGB2, SFPI1, CD101, WAS, FCGR3, CD48, SLC11A1, BCL2A1D, CD86, IL18B3, PLCG2, CXCR1, KLR1, FCER1G, CD4, IL12B, HELLS, RHMO, LPD2	249	219	13588	5.48	8.52E-07	1.42E-07	9.12E-07
GOTERM_BP_FAT	GO:0002774~myeloid leukocyte activation	10	2.89	0.07E-09	PYB, SLC11A1, IL18B3, CXCR1, MYO1F, FCER1G, SFPI1, LPD2, RHMO, FCGR3	249	35	13588	15.59	1.41E-05	1.77E-06	1.51E-05
GOTERM_BP_FAT	GO:0046549~lymphocyte activation	15	4.34	1.09E-05	RORC, ITGB2, SFPI1, CD101, WAS, CD48, SLC11A1, CD86, BCL2A1D, PLCG2, KLR1, CD4, IL12B, HELLS, RHMO	249	191	13588	4.29	1.68E-02	8.46E-04	1.81E-02
Annotation Cluster 6 Category	Enrichment Score: 4.102642809152643 Term	Count <th>%</th> <th>PValue</th> <th>Genes</th> <th>List Total</th> <th>Pop Hits</th> <th>Pop Total</th> <th>Fold Enrichment</th> <th>Benferroni</th> <th>Benjamini</th> <th>FDR</th>	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	21	6.07	1.15E-09	C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, CYP, C1QA, CCL3, CCL31A1, CD83, BCL2A1D, CORO1A, PLCG2, KLRE1, FCER1G, CD4, IL28G, IL12B, CLEC7A, SASH3	249	206	13588	5.56	1.79E-06	2.56E-07	1.92E-06
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	16	4.62	2.64E-08	C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, CYP, C1QA, CCL3, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, 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FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, 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TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B, TUR2, CD101, C1QC, FCGR1, FCGR3, C1QA, CYP, C1QB, CCL31A1, BCL2A1D, PLCG2, KLR1, C4B,							

SLH GO Terms upregulated 504 hours post injury														
Annotation Cluster 1		Enrichment Score: 9.147013030129218		Count	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
Category	Term													
GOTERM_BP_FAT	GO:0006955=inflammatory response	55	7.21	3.31E-12	LVB6, TLR2, H2-D1, C1QC, TLR7, TGFBR1, B2M, CFB, C1RA, CLEC4D, SPON2, DLG3, H2-K1, NCF1, H2-B8, SERPINC1, CLEC4N, C1QA, C1QB, LAT2, CCR5, LILRB3, LILRB4, CCR2, H2-AA, PTM5, CD300B, LCP1, CD300LD, IST1, CCL2, CXCL9, C1QA, C1QB, PFA, C1S, CD74, CCL6, C13A1, FCER1G, PTPN6, PTPRC, CFB, TLR13, MYO1F, H2-AB1, FCGR1, FCGR3, CCL12, ABCG9, FCGR2B, CD300A, H2-EB1, CLEC7A, CCL2, LVB6, TLR2, CXCL9, CCL8, ITGB2, PFA, C1S, C1QC, MDK, TLR7, TGFBR1, CFB, C1RA, C13A1, GPX1, CD44, BCL2, PYCARD, TIRAP, TNFIP2, FN1, PTPN6, GATM, PLXK, CFB, NCF1, TLR13, SERPINC1, ANKRD1, FCGR1, FCGR3, C1QA, C1QB, CCL2, CCR5, NUPR1, STAB1, CCR2, P4207, CLEC7A, CD44, IGFBP4, LCP1, LVB6, H2-D1, TLR2, C1QC, TLR7, TGFBR1, B2M, CFB, C1RA, CD44, DDAG, H2-K1, NCF1, SERPINC1, C1QC, C1QA, C1QB, CCR5, CCR2, PLA2G7, H2-AA, CCL2, CXCL9, CCL8, ITGB2, C1S, CD74, C13A1, BCL2, PYCARD, FCER1G, FN1, PTPN6, PTPRC, UZ2, U2L, CFB, TLR13, MYO1F, COTL1, FCGR1, FCGR3, CCL12, ABCG9, PTPN6, FCGR2B, NUPR1, STAB1, CLEC7A, IGFBP4, CD44, CCL2, LVB6, TLR2, CXCL9, CCL8, ITGB2, C1S, TLR7, C1QC, TGFBR1, CFB, C1RA, C13A1, CD44, PYCARD, FN1, CFB, NCF1, TLR13, SERPINC1, FCGR1, FCGR3, C1QA, C1QB, CCL2, NUPR1, CCR5, STAB1, CCR2, PLA2G7, CLEC7A, CD44, IGFBP4	550	471	13588	2.888	8.17E-09	2.72E-09	5.82E-09		
GOTERM_BP_FAT	GO:0009611=response to wounding	44	5.77	5.00E-11	FCGR1, FCGR3, C1QA, C1QB, CCL2, CCR5, NUPR1, STAB1, CCR2, P4207, CLEC7A, CD44, IGFBP4, LCP1, LVB6, H2-D1, TLR2, C1QC, TLR7, TGFBR1, B2M, CFB, C1RA, CD44, DDAG, H2-K1, NCF1, SERPINC1, C1QC, C1QA, C1QB, CCR5, CCR2, PLA2G7, H2-AA, CCL2, CXCL9, CCL8, ITGB2, C1S, CD74, C13A1, BCL2, PYCARD, FCER1G, FN1, PTPN6, PTPRC, UZ2, U2L, CFB, TLR13, MYO1F, COTL1, FCGR1, FCGR3, CCL12, ABCG9, PTPN6, FCGR2B, NUPR1, STAB1, CLEC7A, IGFBP4, CD44, CCL2, LVB6, TLR2, CXCL9, CCL8, ITGB2, C1S, TLR7, C1QC, TGFBR1, CFB, C1RA, C13A1, CD44, PYCARD, FN1, CFB, NCF1, TLR13, SERPINC1, FCGR1, FCGR3, C1QA, C1QB, CCL2, NUPR1, CCR5, STAB1, CCR2, PLA2G7, CLEC7A, CD44, IGFBP4	550	347	13588	3.13	1.24E-07	2.06E-08	8.80E-08		
GOTERM_BP_FAT	GO:0006952=defense response	51	6.68	5.98E-11	ABCG9, PTPN6, FCGR2B, NUPR1, STAB1, CLEC7A, IGFBP4, CD44, CCL2, LVB6, TLR2, CXCL9, CCL8, ITGB2, C1S, TLR7, C1QC, TGFBR1, CFB, C1RA, C13A1, CD44, PYCARD, FN1, CFB, NCF1, TLR13, SERPINC1, FCGR1, FCGR3, C1QA, C1QB, CCL2, NUPR1, CCR5, STAB1, CCR2, PLA2G7, CLEC7A, CD44, IGFBP4	550	448	13588	2.81	1.48E-07	2.11E-08	1.05E-07		
GOTERM_BP_FAT	GO:0006954=inflammatory response	33	4.33	5.00E-10	PLA2G7, CLEC7A, CD44, IGFBP4	550	225	13588	3.62	1.24E-06	1.37E-07	8.81E-07		
GOTERM_BP_FAT	GO:0002525=immune effector process	24	3.15	1.00E-09	PTPN6, PTPRC, CFB, NCF1, MYO1F, SERPINC1, C1S, TLR7, C1QC, FCGR1, CD74, FCGR3, CFB, C1QA, C1QB, CCL1A1, C1RA, LAT2, ABCG9, FCGR2B, LILRB3, FCER1G, H2-AA, DLG1	550	126	13588	4.71	2.63E-06	2.39E-07	1.87E-06		
GOTERM_BP_FAT	GO:0045087=innate immune response	16	2.10	2.51E-05	PTPN6, CFB, TLR13, TLR2, SERPINC1, C1S, C1QC, FCGR1, TLR7, TGFBR1, CFB, C1QA, C1QB, CCL1A1, H2-K1, UNC93B1, H2-D1, IFI30, H2-DMB1, H2-AB1, FCGR1, CD74, B2M, FCGR3, FCGR2B, H2-EB1, H2-AA, CLEA42, CLEA43, GPNMB, THBS2, FN1, LPHN1, MARC1, PTPRC, IGLA3, CDC80, STAB2, COL5A3, CLEC4N, COLSA1, BGN, ADAMTSR, C6, CLEC12A, STAB1, CLEC3B, C13C3, CLEC3A, FILN7, VCAN, C1QC	550	107	13588	3.69	6.01E-02	1.82E-03	4.41E-02		
Annotation Cluster 2		Enrichment Score: 7.65125481859161		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0030246=carbohydrate binding	39	5.11	7.97E-10	CD1C1	523	317	13288	3.13	5.24E-07	5.24E-07	1.19E-06		
GOTERM_MF_FAT	GO:0005539=glycosaminoglycan binding	21	2.75	1.65E-08	PTPN6, CDC80, CCL8, POSTN, FSTL1, PFA, STAB2, COL5A3, MDK, COLSA1, ADAMTSR, BGN, CD44, C1QC	523	114	13288	4.68	1.08E-05	5.42E-06	2.46E-05		
GOTERM_MF_FAT	GO:0001873=pattern binding	22	2.88	2.47E-08	PTPN6, CDC80, CCL8, POSTN, FSTL1, PFA, STAB2, COL5A3, MDK, COLSA1, ADAMTSR, BGN, CD44, C1QC	523	128	13288	4.37	1.63E-05	5.42E-06	3.70E-05		
GOTERM_MF_FAT	GO:0030247=polysaccharide binding	22	2.88	2.47E-08	PTPN6, CDC80, CCL8, POSTN, FSTL1, PFA, STAB2, COL5A3, MDK, COLSA1, ADAMTSR, BGN, CD44, C1QC	523	128	13288	4.37	1.63E-05	5.42E-06	3.70E-05		
GOTERM_MF_FAT	GO:0008201=heparin binding	16	2.10	6.92E-07	PTPN6, CDC80, CCL8, FSTL1, PFA, POSTN, COLSA3, MDK, COLSA1, ADAMTSR, APOE, FBLN7, PTFN, GPNMB, THBS2, FN1	523	83	13288	4.90	4.55E-04	1.14E-04	1.03E-03		
Annotation Cluster 3		Enrichment Score: 6.147770208479148		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002478=antigen processing and presentation of exogenous peptide antigen	13	1.70	1.51E-11	FCER1G	550	23	13588	13.96	3.74E-08	9.36E-09	2.67E-08		
GOTERM_BP_FAT	GO:0048002=antigen processing and presentation of peptide antigen	15	1.97	2.78E-11	H2-K1, UNC93B1, H2-D1, IFI30, H2-DMB1, H2-AB1, FCGR1, CD74, B2M, FCGR3, C13A1A1, FCGR2B, H2-AA, CLEA7	550	35	13588	10.59	6.88E-08	1.38E-08	4.90E-08		
GOTERM_BP_FAT	GO:0019884=antigen processing and presentation of exogenous antigen	13	1.70	2.83E-10	FCER1G	550	28	13588	11.67	7.00E-08	8.74E-08	4.98E-07		
GOTERM_BP_FAT	GO:0019886=antigen processing and presentation of exogenous peptide antigen via MHC class II	9	1.18	6.52E-08	FCGR2B, H2-EB1, UNC93B1, H2-AA, FCER1G, H2-DMB1, IFI30, H2-AB1, CD74	550	16	13588	13.90	1.61E-04	1.08E-05	1.15E-04		
GOTERM_BP_FAT	GO:0002495=antigen processing and presentation of peptide antigen via MHC class II	9	1.18	6.52E-08	FCGR2B, H2-EB1, UNC93B1, H2-AA, FCER1G, H2-DMB1, IFI30, H2-AB1, CD74	550	16	13588	13.90	1.61E-04	1.08E-05	1.15E-04		
GOTERM_BP_FAT	GO:0002504=antigen processing and presentation of peptide or polysaccharide antigen via MHC class I	9	1.18	3.44E-07	FCGR2B, H2-EB1, UNC93B1, H2-AA, FCER1G, H2-DMB1, IFI30, H2-AB1, CD74	550	19	13588	11.70	5.00E-04	5.00E-05	6.06E-04		
GOTERM_BP_FAT	GO:0019882=antigen processing and presentation	15	1.97	9.34E-06	H2-K1, UNC93B1, H2-D1, IFI30, H2-DMB1, H2-AB1, FCGR1, CD74, B2M, FCGR3, C13A1A1, FCGR2B, H2-AA, CLEA7	550	87	13588	4.26	2.28E-02	7.45E-04	1.65E-02		
Annotation Cluster 4		Enrichment Score: 5.20812368353064		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0002684=positive regulation of immune system process	31	4.06	9.83E-10	ITGAL, STATHS, UNC93B1, TLR2, CACNB3, C1S, C1QC, TGFBR1, CD74, B2M, CFB, C1RA, C13A1A1, HLA, FCER1G, H2-K1, PTPN6, PTPRC, CFB, SERPINC1, FCGR1, FCGR3, TLR7, C1QA, C1QB, CCR5, CDKN1A, LAT2, CDKN1A, H2-AA, CLEC7A	550	206	13588	3.72	2.43E-06	2.43E-07	1.73E-06		
GOTERM_BP_FAT	GO:0002525=immune effector process	24	3.15	1.06E-09	PTPN6, PTPRC, CFB, NCF1, MYO1F, SERPINC1, C1S, TLR7, C1QC, FCGR1, CD74, FCGR3, CFB, C1QA, C1QB, CCL1A1, C1RA, LAT2, ABCG9, FCGR2B, LILRB3, FCER1G, H2-AA, DLG1	550	126	13588	4.71	2.63E-06	2.39E-07	1.87E-06		
GOTERM_BP_FAT	GO:0002443=leukocyte mediated immunity	20	2.62	1.98E-09	PTPN6, NCF1, CFB, PTPN6, PTPRC, C1S, C1QC, FCGR1, CD74, FCGR3, C1QA, C1QB, CCL1A1, C1RA, LAT2, FCGR2B, LILRB3, FCER1G, H2-AA, DLG1	550	89	13588	5.59	4.20E-05	9.48E-07	3.49E-06		
GOTERM_BP_FAT	GO:0005078=positive regulation of immune response	24	3.15	4.98E-09	H2-K1, PTPN6, PTPRC, CFB, STATHS, TLR2, UNC93B1, CACNB3, SERPINC1, C1S, C1QC, FCGR1, FCGR3, H2-B8, B2M, CFB, C1QA, C1QB, CCL1A1, C1RA, LAT2, FCER1G, H2-AA, CLEC7A	550	136	13588	4.36	1.39E-05	4.07E-07	8.77E-06		
GOTERM_BP_FAT	GO:0002449=lymphocyte mediated immunity	17	2.23	4.64E-08	PTPN6, CFB, SERPINC1, C1S, C1QC, FCGR1, CD74, FCGR3, C1QA, C1QB, CCL1A1, C1RA, FCGR2B, LILRB3, FCER1G, H2-AA, DLG1	550	76	13588	5.53	1.15E-04	8.19E-06	8.17E-05		
GOTERM_BP_FAT	GO:0002523=activation of immune response	17	2.23	2.85E-07	PTPN6, PTPRC, CFB, SERPINC1, TLR2, SERPINC1, CACNB3, C1S, C1QC, THY1, CFB, C1QA, C1QB, C1RA, LAT2, FCER1G, CLEC7A	550	86	13588	4.88	7.03E-04	4.40E-05	5.01E-04		
GOTERM_BP_FAT	GO:0048584=positive regulation of response to stimulus	25	3.28	4.79E-07	STATHS, TLR2, UNC93B1, CACNB3, C1S, C1QC, B2M, CFB, C1RA, C13A1A1, FCER1G, H2-K1, PTPN6, PTPRC, CFB, SERPINC1, FCGR1, TLR7, FCER1G, C1QA, C1QB, LAT2, HIRPE, H2-AA, CLEC7A	550	186	13588	3.32	1.18E-03	6.58E-05	8.43E-04		
GOTERM_BP_FAT	GO:0002460=adaptive immune response based on somatic recombination of immune receptors built fr	16	2.10	1.16E-06	FCR1, SERPINC1, C1S, C1QC, FCGR1, CD74, FCGR3, C1QA, C1QB, CCL1A1, C1RA, FCGR2B, LILRB3, CFB, SERPINC1, H2-AA, DLG1	550	84	13588	4.71	2.86E-03	1.43E-04	2.04E-03		
GOTERM_BP_FAT	GO:0002250=adaptive immune response	16	2.10	1.16E-06	FCR1, SERPINC1, C1S, C1QC, FCGR1, CD74, FCGR3, C1QA, C1QB, CCL1A1, C1RA, FCGR2B, LILRB3, CFB, SERPINC1, H2-AA, DLG1	550	84	13588	4.71	2.86E-03	1.43E-04	2.04E-03		
GOTERM_BP_FAT	GO:0019724=B cell mediated immunity	14	1.83	1.58E-06	FCR1, SERPINC1, C1S, C1QC, FCGR1, CD74, FCGR3, C1QA, C1QB, FCGR2B, LILRB3, H2-AA, FCER1G	550	65	13588	5.32	3.90E-03	1.86E-04	2.78E-03		
GOTERM_BP_FAT	GO:0002460=adaptive immune response based on somatic recombination of immune receptors	13	1.70	6.80E-06	FCR1, SERPINC1, C1S, C1QC, FCGR1, CD74, FCGR3, C1QA, C1QB, FCGR2B, H2-AA, FCER1G	550	63	13588	5.30	1.67E-02	5.80E-04	1.20E-02		
GOTERM_BP_FAT	GO:0045087=innate immune response	16	2.10	2.51E-05	C1RA, CLEC7A	550	107	13588	3.69	6.01E-02	1.82E-03	4.41E-02		
Annotation Cluster 5		Enrichment Score: 4.872323284041742		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006348=bone development	18	2.36	5.02E-06	IBSP, IMPA1D, BMP1, MGP, PHL2, SMAD3, IGF2, MMP14, MMP2, CD44, BCL2, ANKRD11, SORT1, PTFN, MYOG, COL3A1, GPNMB, SP1	550	118	13588	3.77	1.23E-02	4.60E-04	8.85E-03		
GOTERM_BP_FAT	GO:0001503=ossification	17	2.23	5.14E-06	IBSP, IMPA1D, BMP1, MGP, SMAD3, PHL2, IGF2, MMP14, MMP2, HDAC3, BCL2, SORT1, PTFN, MYOG, COL3A1, GPNMB, SP1	550	106	13588	3.96	1.26E-02	2.54E-04	9.05E-03		
Annotation Cluster 6		Enrichment Score: 3.660039715600367		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006979=response to oxidative stress	15	1.97	9.34E-06	COL1A1	550	87	13588	4.26	2.28E-02	7.45E-04	1.65E-02		
Annotation Cluster 7		Enrichment Score: 3.05794582612324		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006053=muscle tissue development	19	2.49	9.01E-06	MYH6, ACTC1, RARA, TNC, ELN, DCER1, PHL2, HOMER1, TGFBR1, TNNT2, GPX1, COL3A1A1, EP300, TSC1, H2-K1, UNC93B1, H2-D1, IFI30, H2-DMB1, H2-AB1, FCGR1, CD74, B2M, FCGR3, FCGR2B, H2-EB1, H2-AA, CLEA42, CLEA43, GPNMB, THBS2, FN1, LPHN1, MARC1, PTPRC, IGLA3, CDC80, STAB2, COL5A3, CLEC4N, COLSA1, BGN, ADAMTSR, C6, CLEC12A, STAB1, CLEC3B, C13C3, CLEC3A, FILN7, VCAN, C1QC	550	136	13588	3.45	2.20E-02	7.43E-04	1.59E-02		
GOTERM_BP_FAT	GO:0014706=striated muscle tissue development	18	2.36	1.37E-05	MYH6, ACTC1, RARA, TNC, ELN, DCER1, PHL2, HOMER1, TGFBR1, TNNT2, GPX1, COL3A1A1, EP300, TSC1, H2-K1, UNC93B1, H2-D1, IFI30, H2-DMB1, H2-AB1, FCGR1, CD74, B2M, FCGR3, FCGR2B, H2-EB1, H2-AA, CLEA42, CLEA43, GPNMB, THBS2, FN1, LPHN1, MARC1, PTPRC, IGLA3, CDC80, STAB2, COL5A3, CLEC4N, COLSA1, BGN, ADAMTSR, C6, CLEC12A, STAB1, CLEC3B, C13C3, CLEC3A, FILN7, VCAN, C1QC	550	127	13588	3.50	1.33E-02	1.06E-03	2.41E-02		
Annotation Cluster 8		Enrichment Score: 2.99846280110976		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001775=cell activation	28	3.67	2.38E-06	ITGAL, STATHS, RORC, PFA, SPPL1, ITGB2, TGFBR1, CD74, CD48, SERPINC1A1, CXCR4, BCL2, FCER1G, TNFIP2, DLG1, PFB, PTPRC, PLK4, SMAD3, MYO1F, CDG3, LILRB3, LILRB4, CCR2, H2-AA, CLEA42, CLEA43, GPNMB, THBS2, FN1, LPHN1, MARC1, PTPRC, IGLA3, CDC80, STAB2, COL5A3, CLEC4N, COLSA1, BGN, ADAMTSR, C6, CLEC12A, STAB1, CLEC3B, C13C3, CLEC3A, FILN7, VCAN, C1QC	550	246	13588	2.81	5.86E-03	2.45E-04	4.19E-03		
GOTERM_BP_FAT	GO:0045321=leukocyte activation	24	3.15	2.70E-05	ITGAL, STATHS, RORC, PFA, SPPL1, ITGB2, TGFBR1, CD74, CD48, SERPINC1A1, CXCR4, BCL2, FCER1G, TNFIP2, DLG1, PFB, PTPRC, PLK4, SMAD3, MYO1F, CDG3, LILRB3, LILRB4, CCR2, H2-AA, CLEA42, CLEA43, GPNMB, THBS2, FN1, LPHN1, MARC1, PTPRC, IGLA3, CDC80, STAB2, COL5A3, CLEC4N, COLSA1, BGN, ADAMTSR, C6, CLEC12A, STAB1, CLEC3B, C13C3, CLEC3A, FILN7, VCAN, C1QC	550	219	13588	2.71	6.46E-02	1.91E-03	4.76E-02		
Annotation Cluster 13		Enrichment Score: 2.2378834754282384		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051130=positive regulation of cellular component organization	19	2.49	1.87E-06	ITGAL, STATHS, RORC, PFA, SPPL1, ITGB2, TGFBR1, CD74, CD48, SERPINC1A1, CXCR4, BCL2, FCER1G, TNFIP2, DLG1, PFB, PTPRC, PLK4, SMAD3, MYO1F, CDG3, LILRB3, LILRB4, CCR2, H2-AA, CLEA42, CLEA43, GPNMB, THBS2, FN1, LPHN1, MARC1, PTPRC, IGLA3, CDC80, STAB2, COL5A3, CLEC4N, COLSA1, BGN, ADAMTSR, C6, CLEC12A, STAB1, CLEC3B, C13C3, CLEC3A, FILN7, VCAN, C1QC	550	122	13588	3.85	4.62E-03	2.10E-04	3.30E-03		

Table S3.1 GO Terms upregulated 672 hours post injury													
Annotation Cluster 1	Category	Enrichment Score: 5.942765917628339											
	Term		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benjamini	FDR	
GOTERM_MF_FAT	GO:0005539"glycosaminoglycan binding		23	3.40	8.56E-11	PTPRC, CDCDC8, CCL8, CHOD1, POSTN, PFA, FSTL1, STAB2, DCN, COL5A1, ABIBBP, NCAM1, ADAMTSL, BGN, CD44, APOE, COMP, CFH, FBLN1, GPNMB, FGF2, THSD2, FN1	478	114	13288	5.61	5.13E-08	2.57E-08	1.26E-07
GOTERM_MF_FAT	GO:0010247"polysaccharide binding		24	3.55	1.44E-10	PTPRC, CDCDC8, CCL8, CHOD1, POSTN, PFA, FSTL1, STAB2, DCN, COL5A1, ABIBBP, NCAM1, ADAMTSL, BGN, CD44, APOE, COMP, CFH, FBLN1, GPNMB, FGF2, THSD2, FN1	478	128	13288	5.21	8.65E-08	2.88E-08	2.13E-07
GOTERM_MF_FAT	GO:0001871"pattern binding		24	3.55	1.44E-10	PTPRC, CDCDC8, CCL8, CHOD1, POSTN, PFA, FSTL1, STAB2, DCN, COL5A1, ABIBBP, NCAM1, ADAMTSL, BGN, CD44, APOE, COMP, CFH, FBLN1, GPNMB, FGF2, THSD2, FN1	478	128	13288	5.21	8.65E-08	2.88E-08	2.13E-07
GOTERM_MF_FAT	GO:0010246"carbohydrate binding		38	5.62	2.31E-10	EMCN, GALNT3, CCL8, POSTN, FSTL1, PFA, DCN, CLEC10A, ABIBBP, CD44, APOE, COMP, CFH, CLEC4A2, CLEC4A3, GPNMB, FGF2, SERPFG, THSD2, FN1, LPHN1, MRC1, PTPRC, LGA3L3, CDCDC8, CHOD1, COLEC12, STAB2, COL5A1, CLEC11A, NCAM1, BGN, ADAMTSL, GCK, CLEC12A, CLEC3B, FBLN1, CLEC7A	478	317	13288	3.33	1.39E-07	3.47E-08	3.42E-07
GOTERM_MF_FAT	GO:0008201"heparin binding		18	2.66	4.69E-09	PTPRC, CDCDC8, CCL8, POSTN, FSTL1, PFA, ABIBBP, COL5A1, NCAM1, ADAMTSL, APOE, COMP, FBLN1, CFH, GPNMB, FGF2, THSD2, FN1	478	83	13288	6.03	2.82E-06	5.63E-07	6.93E-06
Annotation Cluster 2	Category	Enrichment Score: 6.07655836906391											
	Term		Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benjamini	FDR	
GOTERM_BP_FAT	GO:0006955"immune response		44	6.66	8.11E-09	LY86, H2-D1, CCL9, CXCL9, APC5, CCL8, PFA, C15, CD1D1, C1QC, CD74, CCL6, B2M, CFH, C1QA, GP4B4, CFB, FCER1G, CLEC4E2, AF215703, C2, SPON2, C2D, PTPRC, CFB, IGJ, H2-DMB1, COLEC12, H2-AB1, SERPING1, FCGR3, C1QA, C1QB, C1QC, CD55, FCGR2B, ULRB3, CCR2, H2-EB1, ULRB4, IL12A, H2-AA, CLEC7A, PTMS, GBL2, LCP1	494	471	13588	2.63	1.79E-05	3.57E-06	1.41E-05
GOTERM_BP_FAT	GO:0009611"response to wounding		37	4.47	1.35E-08	LY86, F13A1, CXCL9, GAL1, CCL8, PFA, C15, C1QC, TRF, CFH, C1QA, GPX1, CD44, BCL2, CFH, C2, CFB, ENTPD2, IGJ, PLEK, CFB, SERPING1, ANKRD3, FCGR3, C1QA, C1C11, C1QB, CD55, SERPINA3, NUPR1, F3, CCR2, PLA2G7, ID3, CLEC7A, PROSL1, LCP1	494	347	13588	2.93	2.96E-05	4.94E-06	2.34E-05
GOTERM_BP_FAT	GO:0002526"acute inflammatory response		17	2.51	2.70E-08	CFB, SERPING1, C15, C1QC, TRF, FCGR3, CFH, C1QA, C1QB, C1QA, CD55, SERPINA3, NUPR1, CFH, C2, CFB, FN1	494	81	13588	5.77	5.93E-05	7.42E-06	4.69E-05
GOTERM_BP_FAT	GO:0002543"activation of plasma proteins involved in acute inflammatory response		12	1.78	3.39E-08	C1QA, CFH, C1QB, C1QA, CD55, CFB, SERPING1, C2, C15, CFB, C1QC	494	36	13588	9.17	7.46E-05	8.29E-06	5.89E-05
GOTERM_BP_FAT	GO:0006956"consolidation of tissue		14	2.07	4.58E-08	C1QA, CFH, C1QB, C1QA, CD55, CFB, SERPING1, C2, C15, CFB, C1QC	494	36	13588	9.17	7.46E-05	8.29E-06	5.89E-05
GOTERM_BP_FAT	GO:0006959"humoral immune response		12	1.78	3.39E-08	C1QA, CFH, C1QB, C1QA, CD55, CFB, SERPING1, C2, C15, CFB, C1QC	494	36	13588	9.17	7.46E-05	8.29E-06	5.89E-05
GOTERM_BP_FAT	GO:0019724"B cell mediated immunity		15	2.22	6.35E-08	CFB, SERPING1, C15, C1QC, CD74, FCGR3, C1QA, C1QB, C1QA, CD55, FCGR2B, ULRB3, H2-AA, FCER1G, C2	494	65	13588	6.35	1.40E-04	1.17E-05	1.10E-04
GOTERM_BP_FAT	GO:0050778"positive regulation of immune response		21	3.11	9.50E-08	PTPRC, CFB, UNC93B1, SERPING1, C15, CD1D1, C1QC, PNP, FCGR3, B2M, CFH, C1QA, C1QB, C1QA, CD55, CFH, FCER1G, H2-AA, C2, CLEC7A, CFB	494	136	13588	4.25	2.09E-04	1.61E-05	1.65E-04
GOTERM_BP_FAT	GO:0002684"regulation of immune system process		26	3.85	1.19E-07	UNC93B1, C15, CD1D1, C1QC, PNP, CFB, B2M, CFH, C1QA, C1QB, C1QA, CD55, IL12A, H2-AA, CLEC7A	494	206	13588	3.47	7.62E-04	1.87E-05	2.07E-04
GOTERM_BP_FAT	GO:0016064"immunoglobulin mediated immune system response		14	2.07	3.21E-07	CFB, SERPING1, C15, C1QC, CD74, FCGR3, C1QA, C1QB, C1QA, CD55, FCGR2B, ULRB3, H2-AA, FCER1G, C2	494	63	13588	6.11	2.06E-04	4.42E-05	5.58E-04
GOTERM_BP_FAT	GO:0002253"activation of immune response		16	2.37	4.08E-07	PTPRC, CFB, UNC93B1, SERPING1, C15, C1QC, CFH, C1QA, C1QB, C1QA, CD55, CFH, FCER1G, CLEC7A, CFB, SERPING1, C15, C1QC, CD74, FCGR3, C1QA, C1QB, C1QA, CD55, FCGR2B, ULRB3, H2-AA, FCER1G, C2	494	86	13588	5.12	8.99E-04	5.29E-05	7.10E-04
GOTERM_BP_FAT	GO:0002449"lymphocyte mediated immunity		15	2.22	4.96E-07	PTPRC, CFB, SERPING1, C15, C1QC, CD74, FCGR3, CFH, C1QA, C1QB, C1QA, CD55, FCGR2B, ULRB3, CFH, FCER1G, H2-AA, C2, CFB	494	76	13588	5.43	0.01092239	6.07E-05	8.63E-04
GOTERM_BP_FAT	GO:0002252"immune effector process		19	2.81	6.47E-07	LY86, H2-D1, CCL9, CXCL9, APC5, CCL8, PFA, C15, CD1D1, C1QC, CD74, TRF, B2M, CFH, C1QA, C1QB, C1QA, CD55, CFH, FCER1G, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY21, NSP, CFB, SERPING1, C1QC, FCGR3, C1C11, C1QA, C1QB, CD55, C2, CFB, FN1, PTPRC, LY2Z, LY2							

Table S2.A KEGG pathways significant at 3 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	49	4.52	2.96E-10	OSMR, CXCR2, IL17RA, TGFBR2, CXCR4, IL1RAP, CSF3R, CSF2RB, IL1B, FAS, IL13RA1, CSF2RA, EGFR, LTBR, INHBB, OSM, TNFRSF10B, PPBP, CCR2, PDGFRA, CXCL1, CSF3, IL1R2, CCL3, IL1R1, CCL2, CSF2RB2, TNFRSF12A, CSF1, CCR1, IL4RA, CXCL2, CXCL9, CCL9, PF4, CNTFR, CCL7, CCL6, CCL24, TNFRSF1A, TNFRSF1B, IL10RA, BMP2, TGFBR1, TGFBR2, CCL11, CXCL14, CXCL16, BMPR1B	434	244	5738	2.66	4.88E-08	4.88E-08	3.59E-07
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	25	2.31	4.36E-09	TNC, COL3A1, SDC4, SDC2, CD44, COMP, COL6A2, COL6A1, COL11A2, THBS1, THBS2, THBS3, THBS4, SPP1, FN1, TNXB, COL4A1, ITGA3, ITGA4, COL5A2, LAMA4, ITGA5, COL1A2, LAMC2, COL1A1	434	83	5738	3.98	7.20E-07	3.60E-07	5.30E-06
KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	22	2.03	7.69E-08	PLAT, C7, C5AR1, MASP1, C3, C4B, CFB, F13A1, SERPING1, C1S, C1QC, PLAUR, C1QA, C1QB, C1RA, THBD, F3, SERPINE1, CFH, CFD, PROS1, PLAU	434	75	5738	3.88	1.27E-05	4.23E-06	9.33E-05
KEGG_PATHWAY	mmu04510:Focal adhesion	37	3.41	4.52E-07	MYL2, PGF, TNC, COL3A1, RAC2, COMP, COL6A2, COL6A1, PIK3R5, ZYX, PAK1, COL11A2, THBS1, THBS2, THBS3, FN1, SPP1, THBS4, ACTB, EGFR, COL4A1, TNXB, ACTN1, ITGA3, ITGA4, FLNC, BIRC3, FLNB, COL5A2, LAMA4, ITGA5, FYN, PDGFRA, COL1A2, RAP1B, LAMC2, COL1A1	434	198	5738	2.47	7.45E-05	1.86E-05	5.48E-04
KEGG_PATHWAY	mmu04210:Apoptosis	22	2.03	1.18E-06	CFLAR, IL1R1, CSF2RB2, RELA, NFKBIA, NFKB1, BIRC3, PRKAR2B, TNFRSF1A, IRAK3, TNFRSF10B, MYD88, RIPK1, IL1RAP, CASP8, CASP12, IL1B, CSF2RB, PIK3R5, FAS, APAF1, MAP3K14	434	87	5738	3.34	1.95E-04	3.89E-05	1.43E-03
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	33	3.04	4.28E-06	CXCL1, ADCY4, CCL3, CCL2, GNAI3, CCR1, CXCL2, CCL9, CXCL9, NFKBIA, NFKB1, CXCR2, PF4, GNG11, CCL7, CCL6, CCL24, RAC2, TIAM1, PTK2B, CXCR4, PIK3R5, PAK1, LYN, RELA, STAT3, STAT2, CCL11, PPBP, CXCL14, CXCL16, CCR2, RAP1B	434	182	5738	2.40	7.05E-04	1.18E-04	5.19E-03
KEGG_PATHWAY	mmu04010:MAPK signaling pathway	41	3.78	1.37E-05	IL1R2, IL1R1, FGFR3, MRAS, DUSP10, HSPA1A, NFKB1, HSPA1B, TGFBR2, FOS, TNFRSF1A, BDNF, RAC2, HSPA2, MAP3K2, MAP3K1, JUND, MAP3K8, IL1B, FAS, PAK1, RAPGEF2, MYC, EGFR, RELA, TGFBR1, TGFBR2, FLNC, FLNB, DUSP5, MAP4K4, DUSP2, GADD45G, NTRK2, PDGFRA, HSPB1, RAP1B, GADD45B, MAP3K14, GADD45A, CD14, PLA2G4E	434	265	5738	2.05	2.26E-03	3.23E-04	1.66E-02

Category	Term
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Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	80	2.10	8.69E-22	ATP5D, UQCRC2, ATP5E, COX11, UQCRC1, COX10, ATP5B, CYC1, NDUFA81, UQCRCF51, COX5A, COX5B, UQCRCQ, NDUFS7, NDUFS6, NDUFS5, UQCRC10, UQCRC11, NDUFS4, NDUFS8, ATP5L, ATP5O, NDUFS3, ATP5H, NDUFS1, ATP5K, ATP5J, COX15, NDUFB10, NDUFC2, COX4D, COX4I, ATP5V2H, NDUFC1, NDUFA10, COX6C, NDUFA11, ATP6V1A, UQCRRH, ATP5C1, UQCRRB, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP6V1B2, ATP5G1, COX7A2L, ATP5G3, NDUFB2, COX6B1, NDUFA4, NDUFA5, NDUFA2, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, NDUFA7, ATP5F1, NDUFA1, PPA2, SDHA, NDUFV3, SDHB, ATP6V02, NDUFV1, SDHC, NDUF2V, SDHD, ATP5A1	1276	130	5738	2.77	1.64E-19	1.64E-19	1.08E-18
					ATP5D, UQCRC2, ATP5E, SNCAIP, UQCRC1, ATP5B, UBE2G1, CYC1, SNCA, NDUFA81, UQCRCF51, COX5A, COX5B, UQCRCQ, NDUFS7, NDUFS6, NDUFS5, CASP3, UQCRC10, UQCRC11, NDUFS4, NDUFS8, ATP5O, NDUFS3, ATP5H, NDUFS1, ATP5K, ATP5J, ATP5I, NDUFB10, SLC25A4, SLC25A5, CYC5, NDUFC2, COX4I2, COX4I1, NDUFC1, NDUFA10, COX6C, UQCRRH, UBC, ATP5C1, UBB, UQCRRB, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP5G1, COX7A2L, ATP5G3, NDUFB2, COX6B1, NDUFA4, NDUFA5, NDUFA2, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, NDUFA7, ATP5F1, UBE2L6, VDACC2, VDACC3, NDUFA1, SDHA, NDUFV3, SDHB, NDUFV1, SDHC, NDUFV2, SDHD, APAF1, ATP5A1	1276	133	5738	2.70	1.24E-18	6.18E-19	8.12E-18
KEGG_PATHWAY	mmu05012:Parkinson's disease	80	2.10	6.54E-21	ATP5D, UQCRC2, ATP5E, CLTB, UQCRC1, ATP5B, CYC1, NDUFA81, REST, CLTC, COX5A, UQCRCF51, COX5B, UQCRCQ, NDUFS7, GPX1, NDUFS6, APB1, NDUFS5, CASP3, UQCRC10, UQCRC11, NDUFS4, NDUFS8, PLCB4, CASP8, NDUFS8, CREB3L2, ATP5O, NDUFS3, ATP5H, NDUFS1, ATP5I, NDUFB10, SLC25A4, SLC25A5, TAF4B, CYC5, NDUFC2, COX4I2, COX4I1, NDUFC1, NDUFA10, COX6C, UQCRRH, ATP5C1, UQCRRB, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP5G1, COX7A2L, ATP5G3, NDUFB2, POLR2A, TFAM, COX6B1, TGM2, TRP53, NDUFA4, NDUFA5, NDUFA2, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, HTT, NDUFA9, DNALC1, NDUFA6, CREBBP, NDUFA7, ATP5F1, VDACC2, VDACC3, NDUFA1, SOD2, NDUFV3, SDHA, SDHB, SP1, BBC3, NDUFV1, SDHC, BAX, NDUFV2, SDHD, APAF1, ATP5A1	1276	133	5738	2.70	1.24E-18	6.18E-19	8.12E-18
					ATP5D, UQCRC2, ATP5E, UQCRC1, ATP5B, SNCA, CYC1, NDUFA81, UQCRCF51, COX5A, COX5B, UQCRCQ, NDUFS7, NDUFS6, NDUFS5, CASP3, UQCRC10, UQCRC11, NDUFS4, PLCB4, CASP8, NDUFS8, ATP5O, FAS, NDUFS3, ATP5H, NDUFS1, ATP5I, NDUFB10, ADAM10, CYC5, NDUFC2, COX4I2, COX4I1, NDUFC1, NDUFA10, CDK5, COX6C, UQCRRH, BACE1, ATP5C1, EIF2AK3, UQCRRB, BID, NDUFB3, NDUFB4, NDUFB5, CDK5R1, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP5G1, COX7A2L, ATP5G3, NDUFB2, TNFRSF1A, COX8B1, GAPDH, NDUFA4, LR, NDUFA5, NDUFA2, COX7A2, NDUFA3, NOS1, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, NDUFA7, ATP5F1, CAPN2, NDUFA1, ITPR2, ADF4, SDHA, NDUFV3, GRP1, RAP1B, DIAP1	1276	182	5738	2.30	2.07E-15	5.17E-16	1.36E-14
KEGG_PATHWAY	mmu05010:Alzheimer's disease	93	2.44	1.09E-17	SDHB, LRPI, ATP2A2, ATP2A3, NDUFV1, SDHC, NDUFV2, CASP12, SDHD, APAF1, ATP5A1, CALM2, PDGFR, PDGFR, PGF, BCFAR1, CHAD, VCL, ACTG1, ARHGAP5, PAK2, PAK4, SHC1, ZYX, COLL1A2, COLL1A1, PKRKA, EGFR, PARVG, ACTN4, BRAF, ROCK1, ROCK2, ACTN1, ACTN2, FLNC, FLNB, FLNA, VASP, VEGFB, CCND1, CCND2, JUN, VEGFA, COL1A2, PDGFR4, LAMC2, LAMC1, COL1A1, CAV3, IBSP, MYL2, TNC, COL3A1, COL2A1, ITGB1, PXN, MYL9, IGF1R, DOCK1, LAMB2, RAC2, COMP, ITGB7, ITGB6, COL6A2, PPP1R12A, COL6A1, PIK3R5, THBS1, THBS2, PIK3R1, THBS3, FLN1, THBS4, SPPI, PIK3R2, ACTB, COL4A2, COL4A1, FLT1, TNXB, MET, BIRC3, CAPN2, COL5A2, VAV1, KDR, VWF, LAMMA, ITGAS, GRP1, RAP1B, DIAP1	1276	182	5738	2.30	2.07E-15	5.17E-16	1.36E-14
					DIST, ACOD2, SLC1G1, CS, IDH3B, ALKY1, DIAT, OGDH, PDHB, IDH3A, SDHA, SDHB, IDH3G, SDHC, DLD, SDHD, IDHD, IDH1, PDHA1, FH1, SLCU2A, MDH2, MDH1	1276	31	5738	3.34	1.76E-07	2.83E-07	1.11E-05
KEGG_PATHWAY	mmu04510:Focal adhesion	23	0.60	8.98E-09	UQCRC2, ATP1B1, UQCRC1, MYL2, ATP1B3, TNNC1, MYL3, ATP1B4, CYC1, COX7B, COX7C, CACNB1, COX7A2L, UQCRCF51, COX5A, COX5B, UQCRCQ, TPMA4, TPMA3, UQCRC10, UQCRC11, COX6B1, ACTC1, SLCB1, COX7A2, COX8B, COX7A1, COX4I2, COX4I1, MYH7, ATP1A1, COX6C, CACNA2D4, ATP2A2, UQCRRH, UQCRRB, SLC9A1	1276	198	5738	1.86	2.76E-07	5.53E-08	1.82E-06
					DIST, ACOD2, SLC1G1, CS, IDH3B, ALKY1, DIAT, OGDH, PDHB, IDH3A, SDHA, SDHB, IDH3G, SDHC, DLD, SDHD, IDHD, IDH1, PDHA1, FH1, SLCU2A, MDH2, MDH1	1276	31	5738	3.34	1.76E-07	2.83E-07	1.11E-05
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	23	0.60	8.98E-09	UQCRC2, ATP1B1, UQCRC1, MYL2, ATP1B3, TNNC1, MYL3, ATP1B4, CYC1, COX7B, COX7C, CACNB1, COX7A2L, UQCRCF51, COX5A, COX5B, UQCRCQ, TPMA4, TPMA3, UQCRC10, UQCRC11, COX6B1, ACTC1, SLCB1, COX7A2, COX8B, COX7A1, COX4I2, COX4I1, MYH7, ATP1A1, COX6C, CACNA2D4, ATP2A2, UQCRRH, UQCRRB, SLC9A1	1276	198	5738	1.86	2.76E-07	5.53E-08	1.82E-06
					DIST, ACOD2, SLC1G1, CS, IDH3B, ALKY1, DIAT, OGDH, PDHB, IDH3A, SDHA, SDHB, IDH3G, SDHC, DLD, SDHD, IDHD, IDH1, PDHA1, FH1, SLCU2A, MDH2, MDH1	1276	31	5738	3.34	1.76E-07	2.83E-07	1.11E-05
KEGG_PATHWAY	mmu04260:Cardiac muscle contraction	37	0.97	2.11E-06	IBSP, TNC, NPNT, COL3A1, COL2A1, SDCA, ITGB1, SDC2, CHAD, LAMB2, CD44, COMP, ITGB7, ITGB6, COL6A2, COL5A1, AGRN, COLL1A2, THBS1, COLL1A1, THBS2, THBS3, FN1, SPP1, THBS4, COL4A2, COL4A4, TNXB, COL5A2, VWF, LAMMA, SDCA1, CD36, ITGAS, COL1A2, LAMC2, LAMC1, COL1A1, BCAT2, EPHA9D, ECHS1, ACAT1, HADHA, HIBADH, AUH, HADHB, MCC2, MPT, MCEE, OXCT1, MCC4, ACAD8, HADH, HMGCL, BCKDHA, ACAA2, ACADN, ACADS, DBT, DLD, AOX1, HIBCH, PKCA, FGFP, PDGFR, PDGFR, PDGFR, NFKB2, NFKB1, PRKX, TGFBR, MAP3K6, FOS, CASP3, MAPK9S, PAK2, B230120E3BK, MAP3K8, FAS, NARF2F2, FGFR2, MYC, CHUK, MAP2K5, PRKCA, EGFR, BRAF, RELB, PTPRR1, ECFST, FLNC, FLNB, FLNA, STK3, MAPK3, MAP4K4, RASGRF2, ARRB2, RRAS2, JUN, GADD45G, PDGFR4, HSPB1, MAPK7, MAP3K14, GADD45B, GADD45A, IL1R2, IL1R1, FGFR3, MKNNK, DUSP10, MAP4K2, CACNB1, HSPA1A, GNG12, HSPA1B, TNFRSF1A, KRAS, HSPA2, RASGRP3, RAC2, ELK4, MAP3K2, PLA2G12A, JUND, RASGRP2, HSPA8, RASA2, PTPN7, TRP53, TGFBR1, TGFBR2, NR4A1, MAPK11, TAB1, CACNA2D4, RP56KA3, DUSP5, NRAS, DUSP4, ATF4, PLA2G4A, RP56KA3, DUSP2, RP56KA4, DUSP1, HSP56A2, NTRK2, RAP1B, PLA2G4B, CD14, DUSP7	1276	78	5738	2.13	3.99E-04	5.70E-05	0.00262723
					IBSP, TNC, NPNT, COL3A1, COL2A1, SDCA, ITGB1, SDC2, CHAD, LAMB2, CD44, COMP, ITGB7, ITGB6, COL6A2, COL5A1, AGRN, COLL1A2, THBS1, COLL1A1, THBS2, THBS3, FN1, SPP1, THBS4, COL4A2, COL4A4, TNXB, COL5A2, VWF, LAMMA, SDCA1, CD36, ITGAS, COL1A2, LAMC2, LAMC1, COL1A1, BCAT2, EPHA9D, ECHS1, ACAT1, HADHA, HIBADH, AUH, HADHB, MCC2, MPT, MCEE, OXCT1, MCC4, ACAD8, HADH, HMGCL, BCKDHA, ACAA2, ACADN, ACADS, DBT, DLD, AOX1, HIBCH, PKCA, FGFP, PDGFR, PDGFR, PDGFR, NFKB2, NFKB1, PRKX, TGFBR, MAP3K6, FOS, CASP3, MAPK9S, PAK2, B230120E3BK, MAP3K8, FAS, NARF2F2, FGFR2, MYC, CHUK, MAP2K5, PRKCA, EGFR, BRAF, RELB, PTPRR1, ECFST, FLNC, FLNB, FLNA, STK3, MAPK3, MAP4K4, RASGRF2, ARRB2, RRAS2, JUN, GADD45G, PDGFR4, HSPB1, MAPK7, MAP3K14, GADD45B, GADD45A, IL1R2, IL1R1, FGFR3, MKNNK, DUSP10, MAP4K2, CACNB1, HSPA1A, GNG12, HSPA1B, TNFRSF1A, KRAS, HSPA2, RASGRP3, RAC2, ELK4, MAP3K2, PLA2G12A, JUND, RASGRP2, HSPA8, RASA2, PTPN7, TRP53, TGFBR1, TGFBR2, NR4A1, MAPK11, TAB1, CACNA2D4, RP56KA3, DUSP5, NRAS, DUSP4, ATF4, PLA2G4A, RP56KA3, DUSP2, RP56KA4, DUSP1, HSP56A2, NTRK2, RAP1B, PLA2G4B, CD14, DUSP7	1276	78	5738	2.13	3.99E-04	5.70E-05	0.00262723
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	38	1.00	4.27E-06	ITGAL, GNAI3, MYL3, GNAI2, MMP9, ICAM1, CD45, ITGB2, ITGB1, MMP2, PIN, ITGAM, VML, MYL9, ACTG1, ARHGAP5, EZR, RAC1, PTK2B, PIK3R5, MSN, PIK3R1, MLT1A, PIK3R2, ACTB, PRKCA, ICAM1, ACTN4, ROCK1, NCF2, NCF1, ROCK2, NCF4, ACTN1, ACTN2, MAPK11, CTNNA1, VAV1, VASP, VTHY1, CYBA, CYBB, RASSF5, PLCG2, GRIP1, RAP1B, JAM2	1276	119	5738	1.78	0.005957607	5.43E-04	0.039252385
					PDGFR, PGF, PDGFA, MMP9, TGFBR3, FOXO1, MMP2, TGFBR1, TGFBR2, SLC2A1, RALB, CSF3R, RARA, FAS, RARB, EGFR, RET, BCR, BRAF, RAR, RXRG, CTNNA1, VEGFR, JUP, HIF1A, JUN, VEGFA, PDGFR4, LAMC2, LAMC1, WNT5A, FGFR3, SPPL1, BCL2L1, ITGB1, KRAS, LAMB2, RAC2, HIF1, RUNX1, AXIN2, CSF1R, FN1, AXIN1, TRP53, BMP4, TCF7, BMP2, EPAS1, TGFBR1, MET, CREBBP, TGFBR2, SMOA3, CRLB, LAMA4, CDKN1A, PLCG2, PPARB, FGFR2, NFKB2, FOS, CCNE1, CASP3, CASP8, FGFR2, MYC, CSF2RA, CHUK, PRKCA, AR, HSP90AA1, CYCS, CDK4, SMO, CCND1, MSMD2, WNT11, WNT9A, BID, PML, KIT, TP53, IGF1R, PIK3R5, PIK3R1, PIK3R2, CEBPA, IL6, COL4A2, COL4A1, MSH2, FZD1, BIRC3, FZD5, STAT3, RALGDS, NRAS, HSP90B1, RASSF5, BAX, RASSF1, JAK1	1276	323	5738	1.43	0.007403353	6.19E-04	0.04881099

Table S2.C KEGG pathways significant at 24 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	76	1.88	2.71E-17	ATP5D, UQCRC2, ATP5E, COX11, COX10, UQCRCF3, COX5A, COX5B, NDUJF57, NDUJF56, NDUJF55, UQCRC10, UQCRC11, NDUFS4, CASP9, APOE, CASP8, NDUFS8, IL1B, ATP5O, NDUFS3, ATP5H, COX17, NDUFS1, ATP5K, ATP5I, NDUFB10, NDUFC2, ATP6V1H, NDUFC1, NDUFA10, ATP6V1D, COX6C, NDUFA11, ATP6V1A, UQCRRH, ATP5C1, UQCRRB, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP5G2, ATP5G1, ATP6V1G1, COX7A2L, NDUFB2, ATP6V0E, COX6B1, TCIRG1, NDUFA4, NDUFA5, NDUFA2, ATP5J2, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, NDUFA7, ATP5F1, LHPP, NDUFA1, PPA2, NDUFV3, ATP6V0E2, ATP6V1E1, SDHC, NDUFV2, SDHD, COX6A2	1355	130	5738	2.48	5.15E-15	5.15E-15	3.37E-14
KEGG_PATHWAY	mmu05010:Alzheimer's disease	87	2.15	1.15E-12	ATP5D, UQCRC2, ATP5E, IDE, COX5A, UQCRCF3, COX5B, NDUJF57, NDUJF56, NDUJF55, APP, CASP3, UQCRC10, UQCRC11, NDUFS4, CASP9, APOE, CASP8, NDUFS8, IL1B, ATP5O, NDUFS3, ATP5H, PLCB2, NDUFS1, ATP5I, NDUFB10, ADAM10, CYCS, NDUFC2, FADD, NDUFC1, NDUFA10, COX6C, UQCRRH, ATP5C1, ERN1, GM12070, EIF2AK3, UQCRRB, BID, NDUFB3, NDUFB4, HSD17B10, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, NME, ATP5G2, ATP5G1, COX7A2L, NDUFB2, TNFRSF1A, COX6B1, PPP3CB, PPP3CA, GAPDH, NDUFA4, NDUFA5, NDUFA2, COX7A2, NDUFA3, NOS1, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, NDUFA7, ATP5F1, CAPN2, NDUFA1, ITPR1, CAPN1, ATF6, NDUFV3, LRPI, ATP2A2, SDHC, NDUFV2, SDHD, COX6A2, CALM3, APAF1, CALM2	1355	182	5738	2.02	2.19E-10	1.09E-10	1.43E-09
KEGG_PATHWAY	mmu05012:Parkinson's disease	69	1.70	3.01E-12	ATP5D, UQCRC2, ATP5E, UBE2G1, UQCRCF3, COX5A, COX5B, NDUJF57, NDUJF56, NDUJF55, UQCRC10, CASP3, UQCRC11, NDUFS4, CASP9, NDUFS8, ATP5O, NDUFS3, ATP5H, NDUFS1, ATP5I, NDUFB10, SLC25A5, CYCS, NDUFC2, NDUFC1, NDUFA10, COX6C, UQCRRH, ATP5C1, UQCRRB, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP5G2, COX7A2L, ATP5G1, NDUFB2, COX6B1, NDUFA4, NDUFA5, NDUFA2, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, NDUFA7, ATP5F1, UBE2L6, VDAC2, VDAC3, NDUFA1, PARK7, VDAC1, NDUFV3, SDHC, NDUFV2, SDHD, COX6A2, APAF1	1355	133	5738	2.20	5.72E-10	1.91E-10	3.74E-09
KEGG_PATHWAY	mmu05016:Huntington's disease	86	2.12	5.05E-12	ATP5D, UQCRC2, ATP5E, CLTA, PPARG, COX5A, UQCRCF3, COX5B, NDUJF57, GPX1, NDUJF56, AP2B1, NDUJF55, CASP3, UQCRC10, UQCRC11, NDUFS4, CASP9, CASP8, NDUFS8, ATP5O, NDUFS3, ATP5H, PLCB2, NDUFS1, ATP5I, NDUFB10, SLC25A5, TAF4B, CYCS, NDUFC2, NDUFC1, NDUFA10, COX6C, UQCRRH, ATP5C1, UQCRRB, POLR2H, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, POLR2K, NDUFB9, POLR2I, COX7B, COX7C, ATP5G2, ATP5G1, COX7A2L, NDUFB2, POLR2A, TFAM, COX6B1, TGM2, TRPS3, NDUFA4, NDUFA5, NDUFA2, COX7A2, NDUFA3, NDUFA8, COX8B, COX7A1, HTT, NDUFA9, NDUFA6, NDUFA7, ATP5F1, VDAC2, VDAC3, NDUFA1, ITPR1, VDAC1, SOD2, NDUFV3, HDAC1, BBC3, SDHC, BAX, NDUFV2, SDHD, COX6A2, APAF1	1355	183	5738	1.99	9.59E-10	2.40E-10	6.27E-09
KEGG_PATHWAY	mmu04210:Apoptosis	45	1.11	3.39E-08	BID, IL1R1, CSF2RB2, NFKBIA, BCL2L1, PRKX, AKT1, IRAK4, PRKAR2B, IRAK3, TNFRSF1A, CASP6, CASP3, MYD88, CASP8, ICCL2, IL1RAP, CASP9B, PPP3CB, CSF2RB, IL1B, PRKACA, PIK3R5, PPP3CA, CHUK, AKT2, IRAK2, TRPS3, PIK3CG, RELA, CYCS, ENDD1, FADD, CAPN2, BIRC3, TRADD, CAPN1, TNFRSF10B, ENDOG, RIRK1, BAX, PRKARIA, APAF1, MAP3K14, IL3RA	1355	87	5738	2.19	6.44E-06	1.29E-06	4.21E-05
KEGG_PATHWAY	mmu04920:Adipocytokine signaling pathway	35	0.86	1.12E-06	PRKAG3, NFKBIE, STK11, NFKBIA, CAMKK1, CAMKK2, AKT1, TNFRSF1A, TNFRSF1B, SLC2A4, SLC2A1, PRKAA1, PRKAA2, ACSL3, CHUK, ACSL6, ACSL5, AKT2, CPT1B, SOCS3, RXRA, RELA, PRKAB2, PRKAB1, RXRG, ADIPOR1, ACACB, ADIPOQ, IRS1, CPT1A, STAT3, TRADD, PRKCG, NPY, JAK2, MARKCSL1, WASF2, ASAP1, ARPC4, ARF6, ARPC5, AKT1, DOCK2, RAC2, ARPC3, GAB2, ARPC2, GSN, PIKFYVE, PIK3R5, INPP5D, PAK1, AKT2, PRKCA, PIK3CG, PTPRCB, VAV3, LYN, PPA2P2, LIMK1, NCF1, HCK, SPHK1, PRKCE, FCGR1, WAS, VAV1, PRKCB, VASP, PRKCB, ARPC1B, PLA2G4A, FCGR2B, ARPC5L, CFL1, PLCG2, SCIN, MARCKS, PLA2G4E	1355	67	5738	2.21	2.13E-04	3.55E-05	0.001393144
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	44	1.09	6.54E-06	ADCY2, ADCY7, PREX1, STAT5B, CXCR2, PRKX, AKT1, TIAM2, CXCR4, TIAM1, RHOA, PRKACA, SHC1, PAK1, CSK, PLCB2, CHUK, AKT2, PIK3CG, LYN, NCF1, RELA, IRAK, PRKCD, HRAS1, PRKCB, ELMO1, GNB2, PP8P, CCR5, ARRB2, GNB1, CCR2, CX3CR1, GNB5, CXCL1, PARO3, CCL3, GNAI3, CCL2, GNAI2, FGR, CCR1, CCL9, NFKBIA, CCL8, PF4, CCL7, CCL6, CCL24, CCL25, DOCK2, KRAS, RAC2, PTK2B, SOS2, PIK3R5, VAV3, HCK, VAV1, STAT3, STAT2, NRAS, CCL12, CXCL14, GNG10, CXCL16, JAK2, RAP1B, GRK5, BID, STEAP3, CHEK1, SFN, RRM2B, PMAIP1, CCGN1, SESN2, CCGN2, CCNE1, CASP3, CASP9, SHISA5, SERPINE1, CASP8, THBS1, TRPS3, CDK1, CYCS, CDK6, CDK4, CDK2, RFWO2, CCND1, CDKN1A, EIZ4, BDC3, CCND2, CD82, RRM2, BAX, GADD45G, APAF1, GADD45A	1355	98	5738	1.90	0.001241374	1.77E-04	0.00812502
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	70	1.73	7.95E-06	ADCY2, ADCY7, PREX1, STAT5B, CXCR2, PRKX, AKT1, TIAM2, CXCR4, TIAM1, RHOA, PRKACA, SHC1, PAK1, CSK, PLCB2, CHUK, AKT2, PIK3CG, LYN, NCF1, RELA, IRAK, PRKCD, HRAS1, PRKCB, ELMO1, GNB2, PP8P, CCR5, ARRB2, GNB1, CCR2, CX3CR1, GNB5, CXCL1, PARO3, CCL3, GNAI3, CCL2, GNAI2, FGR, CCR1, CCL9, NFKBIA, CCL8, PF4, CCL7, CCL6, CCL24, CCL25, DOCK2, KRAS, RAC2, PTK2B, SOS2, PIK3R5, VAV3, HCK, VAV1, STAT3, STAT2, NRAS, CCL12, CXCL14, GNG10, CXCL16, JAK2, RAP1B, GRK5, BID, STEAP3, CHEK1, SFN, RRM2B, PMAIP1, CCGN1, SESN2, CCGN2, CCNE1, CASP3, CASP9, SHISA5, SERPINE1, CASP8, THBS1, TRPS3, CDK1, CYCS, CDK6, CDK4, CDK2, RFWO2, CCND1, CDKN1A, EIZ4, BDC3, CCND2, CD82, RRM2, BAX, GADD45G, APAF1, GADD45A	1355	182	5738	1.63	0.001508532	1.89E-04	0.009874856
KEGG_PATHWAY	mmu04115:p53 signaling pathway	34	0.84	8.49E-06	ADCY2, ADCY7, PREX1, STAT5B, CXCR2, PRKX, AKT1, TIAM2, CXCR4, TIAM1, RHOA, PRKACA, SHC1, PAK1, CSK, PLCB2, CHUK, AKT2, PIK3CG, LYN, NCF1, RELA, IRAK, PRKCD, HRAS1, PRKCB, ELMO1, GNB2, PP8P, CCR5, ARRB2, GNB1, CCR2, CX3CR1, GNB5, CXCL1, PARO3, CCL3, GNAI3, CCL2, GNAI2, FGR, CCR1, CCL9, NFKBIA, CCL8, PF4, CCL7, CCL6, CCL24, CCL25, DOCK2, KRAS, RAC2, PTK2B, SOS2, PIK3R5, VAV3, HCK, VAV1, STAT3, STAT2, NRAS, CCL12, CXCL14, GNG10, CXCL16, JAK2, RAP1B, GRK5, BID, STEAP3, CHEK1, SFN, RRM2B, PMAIP1, CCGN1, SESN2, CCGN2, CCNE1, CASP3, CASP9, SHISA5, SERPINE1, CASP8, THBS1, TRPS3, CDK1, CYCS, CDK6, CDK4, CDK2, RFWO2, CCND1, CDKN1A, EIZ4, BDC3, CCND2, CD82, RRM2, BAX, GADD45G, APAF1, GADD45A	1355	69	5738	2.09	0.001611612	1.79E-04	0.010550125
KEGG_PATHWAY	mmu00230:Purine metabolism	62	1.53	1.10E-05	GDA, ADCY2, GMPR2, ADCY7, PDE3B, PNP, PRIM1, NTSM, NTS5C3, PDE4A, PRIM2, NTS5C2, IMPDH1, NTS5, NTS5, NUDT2, POLR1E, NUDT5, PDE4D, PDE10A, POLR1B, GMPR, NME1, ADK, RRM2, ADSL, PRPS2, XDH, POLR2H, ADSS, ENPP1, POLR2K, NTS5C1A, POLR2I, POLA1, DCK, RRM2B, PFAS, ADA, POLR2A, POLE2, PDE1B, ATIC, NUDT9, ENTPD4, ENTPD1, PAPSS1, PAPSS2, ADSL1, AK1, POLR3GL, NRP2, AMPD2, AMPD1, APRT, POLR3D, AMPD1, POLD1, PDE7B, PDE2A, POLD1, PAICS, PFOS2, PGF, MAPP, STAT5B, FGF13, TGFBI, WNTA, SLC2A1, RALU, CSF3R, RARA, RARB, EGFR, PIK3CG, BCR, RXRA, RELA, RXRG, SREBP, FADD, CTNNA1, STK4, CTNNA3, HRAS1, VEGFB, CCDC6, HIF1A, VEGFA, PDGFRA, LAMC2, TRAF1, NFKBIA, SFP1, BCL2L1, ITGB1, RBX1, LAMB2, KRAS, RAC2, FH1, RUNX1, CSF1R, FN1, TRPS3, BMP2, EPAS1, MAP2K2, SMAD3, ITGA3, CDKN1A, CDKN1B, HDAC1, PLCG2, E2F1, PPARG, NFKB2, AKT1, ACVR1B, CCNE1, FOS, CASP3, CASP9, CASP8, RHOA, MYC, CHUK, CSF2RA, AKT2, PRKCA, AR, HSP90AA1, CYCS, CDK6, CDK4, CDK2, PRKCB, DAPK1, SMO, CCND1, WNT11, WNT9A, BID, CCK1B, PML, EGR2, KIT, ZBTB16, TPX3, HGFIR, BCL2, SOS2, PIK3R5, CEBPA, IL6, CDL4A2, CDL4A1, VHL, CBL, BIRC3, FZD5, FZD4, STAT3, FZD7, NRAS, HSP90B1, RASSF5, BAX, RASSF1, ARAF	1355	157	5738	1.67	0.00208012	2.08E-04	0.013620114
KEGG_PATHWAY	mmu05200:Pathways in cancer	109	2.69	2.31E-05	GDA, ADCY2, GMPR2, ADCY7, PDE3B, PNP, PRIM1, NTSM, NTS5C3, PDE4A, PRIM2, NTS5C2, IMPDH1, NTS5, NTS5, NUDT2, POLR1E, NUDT5, PDE4D, PDE10A, POLR1B, GMPR, NME1, ADK, RRM2, ADSL, PRPS2, XDH, POLR2H, ADSS, ENPP1, POLR2K, NTS5C1A, POLR2I, POLA1, DCK, RRM2B, PFAS, ADA, POLR2A, POLE2, PDE1B, ATIC, NUDT9, ENTPD4, ENTPD1, PAPSS1, PAPSS2, ADSL1, AK1, POLR3GL, NRP2, AMPD2, AMPD1, APRT, POLR3D, AMPD1, POLD1, PDE7B, PDE2A, POLD1, PAICS, PFOS2, PGF, MAPP, STAT5B, FGF13, TGFBI, WNTA, SLC2A1, RALU, CSF3R, RARA, RARB, EGFR, PIK3CG, BCR, RXRA, RELA, RXRG, SREBP, FADD, CTNNA1, STK4, CTNNA3, HRAS1, VEGFB, CCDC6, HIF1A, VEGFA, PDGFRA, LAMC2, TRAF1, NFKBIA, SFP1, BCL2L1, ITGB1, RBX1, LAMB2, KRAS, RAC2, FH1, RUNX1, CSF1R, FN1, TRPS3, BMP2, EPAS1, MAP2K2, SMAD3, ITGA3, CDKN1A, CDKN1B, HDAC1, PLCG2, E2F1, PPARG, NFKB2, AKT1, ACVR1B, CCNE1, FOS, CASP3, CASP9, CASP8, RHOA, MYC, CHUK, CSF2RA, AKT2, PRKCA, AR, HSP90AA1, CYCS, CDK6, CDK4, CDK2, PRKCB, DAPK1, SMO, CCND1, WNT11, WNT9A, BID, CCK1B, PML, EGR2, KIT, ZBTB16, TPX3, HGFIR, BCL2, SOS2, PIK3R5, CEBPA, IL6, CDL4A2, CDL4A1, VHL, CBL, BIRC3, FZD5, FZD4, STAT3, FZD7, NRAS, HSP90B1, RASSF5, BAX, RASSF1, ARAF	1355	323	5738	1.43	0.004375503	3.99E-04	0.028680546



Table S2.D KEGG pathways significant at 48 hours												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu00280:Valine, leucine and isoleucine degradation	28	1.30	2.79E-12	BCAT1, ACAD5B, BCAT2, ECHS1, ACAT1, HIBADH, HADHA, AUH, HADHB, MCCC2, MUT, IVO, MCCC1, MCEE, OXCT1, HADH, BCKDHA, ACAA2, ALDH6A1, ACADM, ACADS, BCKDHB, DBT, DLD, ALDH2, PCCB, ALDH9A1, PCCA	820	46	5738	4.26	4.99E-10	4.99E-10	3.43E-09
KEGG_PATHWAY	mmu05010:Alzheimer's disease	55	2.56	4.10E-08	UQCRC2, UQCRC1, CYC1, NDUFA81, UQCRCF1, NDUFS7, CASP3, NDUFS4, UQCRC11, CASP9, APOE, NDUFS8, CASP8, IL1B, NDUFS3, PLCB2, NDUFS2, NDUFS1, ADAM10, NDUFB10, CYCS, NDUFC1, NDUFA10, ATP5C1, UQCRC8, NDUFB3, BID, CDK5R1, TM4SF19, NDUFB8, NDUFB9, NDUFB2, TNFRSF1A, PPP3CB, PPP3CA, LPL, NDUFA5, NOS1, COX7A1, COX8B, NDUFA8, NDUFA9, NDUFA6, CACNA1S, SDHA, NDUFV3, SDHB, LRP1, ATP2A2, NDUFV1, SDHC, NDUFV2, COX6A2, COX6A1, APAF1	820	182	5738	2.11	7.33E-06	3.67E-06	5.04E-05
KEGG_PATHWAY	mmu05012:Parkinson's disease	44	2.05	6.92E-08	UQCRC2, NDUFB3, UQCRC1, NDUFB8, NDUFB9, CYC1, UCHL1, NDUFA81, PINK1, UQCRCF1, NDUFB2, NDUFS7, CASP3, UQCRC11, NDUFS4, CASP9, NDUFS8, NDUFS3, NDUFS2, NDUFS1, NDUFA5, NDUFB10, NDUFA8, COX8B, COX7A1, NDUFA9, SLC25A5, NDUFA6, NDUFC1, NDUFA10, VDAC3, VDAC1, NDUFV3, SDHA, SDHB, NDUFV1, SDHC, NDUFV2, COX6A2, ATP5C1, COX6A1, APAF1, UQCRCB, ITGAL, GNAI3, MYL2, GNAI2, MMP9, ITGB2, ITGAM, VCL, ACTG1, VCAM1, EZR, RAC2, PTK2B, CXCR4, RHOA, PIK3R5, MSN, RHOH, ACTB, PRKCA, PIK3CG, ICAM1, VAV3, NCF2, ACTN4, NCF1, NCF4, ACTN1, MYL12B, VAV1, VASP, THY1, PRKCB, CYBA, CYBB, RASSF5, MAPK12, PLCG2, RAP1B	820	133	5738	2.31	1.24E-05	4.13E-06	8.52E-05
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	39	1.81	5.77E-07	UQCRC2, NDUFB3, UQCRC1, NDUFB8, NDUFB9, CYC1, NDUFA81, UQCRCF1, NDUFB2, NDUFS7, ATP6VOE, UQCRC11, NDUFS4, NDUFS8, NDUFS3, NDUFS2, NDUFS1, ATP5K, TCIRG1, NDUFA5, NDUFB10, NDUFA8, COX8B, COX7A1, NDUFA9, NDUFA6, ATP6V1H, NDUFC1, NDUFA10, NDUFV3, SDHA, SDHB, ATP6V1A, ATP6VOE2, NDUFV1, SDHC, NDUFV2, COX6A2, ATP5C1, COX6A1, UQCRCB, SUCLG1, CS, IDH3B, ACLY, DLAT, OGDH, IDH3A, SDHA, SDHB, IDH3G, SDHC, DLD, IDH2, PDHA1, FH1, SUCLA2, MDH1	820	130	5738	2.21	1.55E-04	3.10E-05	0.001065029
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	17	0.79	9.45E-07	MARCKS1, ARPC4, ARF6, APC2, DOCK2, RAC2, ARPC3, GAB2, ARPC2, PIK3R5, INPP5D, PIK3CG, PRKCA, PTPRC, VAV3, LYN, PPAP2C, NCF1, LIMK1, HCK, SPHK1, VAV1, PRKCD, WAS, FCGR1, VASP, ARPC18, PLA2G4A, FCGR2B, CFL1, PLCG2, MARCKS	820	31	5738	3.84	1.69E-04	2.82E-05	0.001162609
KEGG_PATHWAY	mmu04666:Fc gamma R-mediated phagocytosis	33	1.53	2.63E-06	PRKCB, ARPC18, PLA2G4A, FCGR2B, CFL1, PLCG2, MARCKS	820	98	5738	2.36	4.71E-04	6.72E-05	0.0032361
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	49	2.28	9.62E-06	ADCY7, STAT5B, CXCR2, PRKX, CXCR4, RHOA, CSK, PLCB2, PIK3CG, LYN, NCF1, PRKCD, WAS, ELMO1, PRKCB, CCR5, PPBP, ARRB2, GNB1, CX3CR1, CCR2, GNAI3, CCL2, GNAI2, FGR, CCR1, CCL9, CCL8, PF4, CCL4, CCL7, CCL6, DOCK2, RAC2, PTK2B, SOS2, PIK3R5, VAV3, HCK, VAV1, STAT3, NRAS, ADCY9, CXCL14, CXCL13, CXCL16, GNG10, JAK2, RAP1B	820	182	5738	1.88	0.001720856	2.15E-04	0.011840157
KEGG_PATHWAY	mmu05016:Huntington's disease	49	2.28	1.13E-05	UQCRC2, CLTA, UQCRC1, CYC1, NDUFA81, UQCRCF1, NDUFS7, GPX1, CASP3, NDUFS4, UQCRC11, CASP9, NDUFS8, CASP8, NDUFS3, PLCB2, NDUFS2, NDUFS1, NDUFB10, SLC25A5, CYCS, NDUFC1, NDUFA10, ATP5C1, UQCRC8, NDUFB3, NDUFB8, NDUFB9, NDUFB2, TRP53, NDUFA5, COX7A1, COX8B, NDUFA8, NDUFA9, NDUFA6, VDAC3, SOD2, VDAC1, SDHA, NDUFV3, SDHB, BAX, SDHC, NDUFV1, NDUFV2, COX6A2, COX6A1, APAF1	820	183	5738	1.87	0.002020134	2.25E-04	0.013901248
KEGG_PATHWAY	mmu00640:Propanoate metabolism	15	0.70	2.05E-05	ALDH6A1, LDHB, ACADM, SUCLG1, ECHS1, ACAT1, HADHA, MUT, ACS1, MCEE, ALDH2, SUCLA2, PCCB, ALDH9A1, PCCA	820	30	5738	3.50	0.003656954	3.66E-04	0.025184004

Table S2.E KEGG pathways significant at 72 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu05010:Alzheimer's disease	125	1.73	1.05E-16	ID4, SNCA, NDUFA81, COX5A, COX5B, APP, UQCRC10, UQCRC11, APOE, IL1B, PSENEN, FADD, COX6C, BACE2, MAPK3, ATP5C1, GM12070, EIF2AK3, HSD17B10, CDK5R1, COX7B, COX7C, MME, COX6B1, COX6B2, LPL, COX8B, COX8A, CACNA1S, NDUFV3, ATP2A2, ATP2A3, NDUFV1, NDUFV2, COX6A2, COX6A1, CACNA10, ATP50, UQCRC2, ATP5E, UQCRC1, ATP5B, CYC1, UQCRCF51, UQCRCQ, NDUFS7, NDUFS6, NDUFS5, CASP3, PLCB3, NDUFS4, CASP9, CASP7, MAPT, CASP8, NDUFS8, ATP50, NDUFS3, PLCB1, NDUFS2, ATP5H, PLCB2, NDUFS1, ATP5I, NDUFB10, ADAM10, CYC5, NDUFC2, COX4I2, COX4I1, NDUFC1, NDUFA10, GNAQ, UQCRR, PSEN2, ADAM17, UQCRR, BID, NDUFB3, NDUFB4, NDUFB5, NDUFB6, TNF, NDUFB7, NDUFB8, NDUFB9, ADPH1C, PPP3R1, ATP5G2, ATP5G1, COX7A2L, ATP5G3, NDUFB2, TNFRSF1A, PPP3CB, PPP3CC, PPP3CA, GAPDH, NDUFAA, NDUFA5, NDUFA2, NOS1, COX7A8, NDUFA3, COX7A1, NDUFA8, NDUFA9, NDUFA6, NDUFA7, ATP5F1, CAPN2, ITPR3, NDUFA1, ITPR1, CAPN1, ITPR2, NAE1, SDHA, SDHB, LRP1, GSK3B, SDHC, SDHD, CALM3, ATP5A1, APAF1	2203	182	5738	1.79	2.14E-14	2.14E-14	1.33E-13
					ATP5D, UQCRC2, ATP5E, COX11, UQCRC1, COX10, ATP5B, CYC1, NDUFA81, COX5A, UQCRCF51, COX5B, UQCRCQ, NDUFS7, NDUFS6, NDUFS5, UQCRC10, UQCRC11, NDUFA5, NDUFS8, ATP5L, ATP50, ATP6VD01, NDUFS3, NDUFS2, ATP6VD02, ATP5H, COX17, NDUFS1, ATP5K, ATP5J, NDUFB10, NDUFC2, COX4I2, COX4I1, ATP6V1H, NDUFC1, NDUFA10, ATP6V1D, COX6C, NDUFA11, ATP6V1A, UQCRR, ATP5C1, UQCRR, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, COX7C, ATP5G2, ATP5G1, ATP6VC02, ATP6V1G1, COX7A2L, ATP5G3, NDUFB2, ATP6V0E, COX6B1, COX6B2, TCIRG1, NDUFA4, NDUFA5, NDUFA2, ATP5I2, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, COX8A, NDUFA7, ATP5F1, LHPP, NDUFA1, PPA2, SDHA, NDUFV3, SDHB, ATP6V0E2, NDUFV1, ATP6V1E1, SDHC, NDUFV2, SDHD, COX6A2, COX6A1,	2203	130	5738	1.90	4.07E-13	2.04E-13	2.63E-12
KEGG_PATHWAY	mmu05016:Huntington's disease	123	1.71	3.38E-15	NDUFA81, COX5A, COX5B, BDNF, UQCRC10, UQCRC11, CREB3L1, CREB3L4, CREB3L3, RCOR1, PPARGC1A, COX6C, ATP5C1, COX7B, COX7C, COX6B1, COX6B2, HIP1, TRPS3, COX8B, HTT, COX8A, VDACC2, VDACC3, VDACC1, NDUFV3, HDACC2, HDACC1, BBC3, NDUFV1, PPID, NDUFV2, COX6A2, COX6A1, ATP5D, UQCRC2, ATP5E, CLTA, UQCRC1, CLTB, AP2S1, ATP5B, CYC1, PPARG, CLTC, UQCRCF51, UQCRCQ, NDUFS7, NDUFS6, GPN1, AP2B1, NDUFS5, CASP3, PLCB3, NDUFS4, CASP9, CASP8, NDUFS8, DLGA4, ATP5D, NDUFS3, PLCB1, NDUFS2, ATP5H, PLCB2, NDUFS1, ATP5I, NDUFB10, SLC25A4, SLC25A5, CYC5, NDUFC2, COX4I2, COX4I1, NDUFC1, NDUFA10, GNAQ, UQCRR, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, POLR2L, POLR2I, ATP5G2, ATP5G1, COX7A2L, ATP5G3, POLR2C, NDUFB2, POLR2A, TFAM, NDUFA4, NDUFA5, NDUFA2, COX7A2, NDUFA3, NDUFA8, COX7A1, NDUFA9, NDUFA6, NDUFA7, ATP5F1, CREB5, NDUFA1, ITPR1, SOD2, SDHA, SODH, AP2A2, SPI1, IFT57, BAK, SDHC, SDHD, APAF1, ATP5A1	2203	183	5738	1.75	6.43E-13	2.14E-13	4.15E-12
					ATP5D, UQCRC2, ATP5E, UQCRC1, ATP5B, UBE2G1, SNCA, UCHL1, CYC1, NDUFA81, PINK1, COX5A, UQCRCF51, COX5B, UQCRCQ, NDUFS7, NDUFS6, NDUFS5, CASP3, UQCRC10, UQCRC11, NDUFS4, HTRA2, CASP9, NDUFS8, ATP5D, NDUFS3, NDUFS2, ATP5H, NDUFS1, ATP5I, NDUFB10, SLC25A4, SLC25A5, CYC5, NDUFC2, COX4I2, COX4I1, NDUFC1, NDUFA10, COX6C, UQCRR, UBC, ATP5C1, UBA52, UQCRR8, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, COX7B, UBA7, COX7C, ATP5G2, ATP5G1, COX7A2L, ATP5G3, NDUFB2, COX6B1, COX6B2, NDUFA4, NDUFA5, NDUFA2, COX7A2, NDUFA3, NDUFA8, COX7A1, COX8B, NDUFA9, NDUFA6, COX8A, NDUFA7, ATP5F1, UBE2L6, VDACC2, VDACC3, NDUFA1, PARK7, VDACC1, SDHA, NDUFV3, SDHB, NDUFV1, SDHC, NDUFV2, SDHD,	2203	119	5738	1.66	6.53E-06	9.33E-07	4.22E-05
KEGG_PATHWAY	mmu05012:Parkinson's disease	94	1.30	8.90E-14	COX6A2, SLC18A2, COX6A1, APAF1, ATP5A1	2203	133	5738	1.84	1.72E-11	4.29E-12	1.11E-10
					OGDH, PDH1B, IDH3G, IDH2, IDH1, FH1, CSL, PDHA1, SUCCLA2, DLST, ACO2, SUCLG2, ACO1, SUCLG1, CS, IDH3B, ACILY, DLAT, PKC2, IDH3A, SDHA, SDHB, PCX, SDHC, DLD, SDHD, MDH2, MDH1	2203	31	5738	2.35	5.20E-06	1.04E-06	3.36E-05
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	28	0.39	2.69E-08	TBK1, TLRI, TRAP, TLR2, TLR3, NFKB1, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, AKT1, MAP3K7, FOS, MYD88, TICAM1, CASP8, MAP3K8, TICAM2, IL1B, PIK3CA, LBP, MAP2K7, AKT3, MAP2K6, AKT2, PIK3CG, LY96, REL, PIK3CD, FADD, CD40, IFNAR1, IFNAR2, CD86, CD80, JUN, RIKP1, MAPK3, IL12A, MAPK9, MAPK8, CCL3, TNF, CXCL5, NFKBIA, CCL5, CCL4, IRAK4, PIK3RS, SPP1, IL6, MAP2K2, MAP2K3, MAP2K4, MAPK11, STAT1, TAB2, IKKKE, IRF5, MAPK12, IRF7, MAPK14, IKKBK, CD14	2203	99	5738	1.74	5.37E-06	8.96E-07	3.47E-05
					SGSH, ARSB, CLTA, CLTB, GM2A, AP1B1, HEXA, LGMN, HEXB, AP3S1, CLTC, ASAHI, GLB1, AP1S3, AP1S1, AP1S2, ATP6VD01, MAN2B1, ATP6VD02, AP3B1, CLN3, HYALL1, CT52, ATP6V1H, NAPSAC, CTSS, MEPR, DNASE2A, CTSW, GNS, CTSB, CTSK, CTSD, GAA, CTSD, NEU1, CTSC, CTSB, CTSF, AP1M1, NAGLU, MFSDB, ACPS, PPT1, CTSB, ACP2, ATP6VC02, SLC11A1, CD68, NAGPA, LAPTM5, AP3M2, GALNS, NAGA, GALT, AP3D1, ENTPD4, GBA, LAPTM4B, TCIRG1, ABCB9, PLA2G15, UPA, PSAP, GUSB,	2203	62	5738	1.93	7.98E-06	9.97E-07	5.15E-05
KEGG_PATHWAY	mmu04621:NOD-like receptor signaling pathway	46	0.64	4.13E-08	CD63, FUCAI, MANBA, SLC17A5, LAMP2, GLA, ARSA, SMPD1, CTNS, GGA2, CXCL1, TNF, CCL1, IL18, NFKBIB, CCL8, CXCR4, NFKB1A, CXCL11, CCL5, CCL4, CCL7, CCL6, CDK2, RAC2, NLRCA, NOD2, NOD1, MEV1, NAI2, CASP8, NAIIPS, PSTPIP1, PYCARD, IL1B, CASP1, IL6, HSP90AA1, CARD9, RELB, MAPK11, CARD6, SUGT1, BIRC3, BIRC2, TAB2, CCL12, HSP90B1, MAPK12, MAPK14, MAPK3, RIPK2, MAPK9, MAPK8, TNFAIP3, TRIP6, IKKBK	2203	62	5738	1.93	7.98E-06	9.97E-07	5.15E-05
					ADCY3, ADCY1, ADCY2, ADCY7, STAT5B, CXCL12, PRKX, PIK3CA, GNG2, GNG5, GNG7, PIK3CG, ROCK1, ROCK2, NCF1, REL, PIK3CD, HRAS1, CCR7, PPPR, CCNS, ARRB2, CCR2, CXCR1, MAPK3, CCL3, GNAI3, CCL2, GNAQ2, FGR, GRB2, NFKBIB, CCL8, CXCR4, NFKB1A, CXCL11, CCL5, CCL4, CCL7, CCL6, CDK2, RAC2, VAV2, VAV1, VAV1L, CXCL14, CXCL13, CXCL16, GRK6, GRK4, RAP1B, GRK5, IKKBK, PREX1, NFKB1, CXCR2, CXCR3, AKT1, PLCB3, CXCR4, RHOA, SHC1, PLCB1, CSK, PLCB2, AKT3, AKT2, LYN, WAS, PRKCD, PRKCB, ELMO1, GNB2, GNB1, GNB5, GNB4, GNB3, CXCL1, PARO3, CXCL5, CCR1, CXCL9, PF4, GNG11, GNG12, CCL28, CCL24, CCL25, CCL22, PRK2, SOD1, SOD2, PIK3R5, HCK, RAF1, STAT1, STAT3, STAT2,	2203	182	5738	1.52	1.25E-05	1.39E-06	8.08E-05
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	106	1.47	6.48E-08	NKAS, CCL12, ADCY9, GSK3A, GSK3B, GNG10, JAK3, MEK2, FGFR1, PDGFA, GNAI2, FGFR3, TGFBR1, PRKX, TGFBR2, MAP3K7, MAP3K6, BDNF, MAP3K4, B230120H23R6, MAP3K8, IL1B, RRAS, MAP2K7, MAP2K6, EGFR, RELB, REL, PTPRR, MECOM, STK4, STK3, HRAS1, MAP4K4, ARRB2, JUN, MAPK3, PDGFRA, HSPB1, MAPK9, MAPK8, MAPK7, STMN1, PLA2G2E, NGF, PPP5C, IL1R2, FGFR4, IL1R1, FGFR3, GRB2, MAPKAPK5, CACNB1, DUSP10, MAP4K1, CACNB3, MAPKAPK2, HSPA1B, SRF, HSPA1L, RAC2, DUSP14, RAC3, JUND, DUSP16, EGF, PTPN7, TRPS3, CACNA2D1, NTF5, NTF3, MAP2K2, MAP2K3, TGFBR1, TGFBR2, MAP2K4, TAOK3, NR4A1, CACNA1S, CACNA2D4, AT1A, PLA2G4A, RAP1B, IKKBK, CACNA10, CACNA1A, PLA2G4E, FGFR, NFKB1, NFKB2, DAXX, AKT1, ACVR1B, FOS, MAX, CASP3, PAK2, MAPT, MYC, AKT3, AKT2, PRKCA, CACNG7, CACNG6, CACNG1, ECFST, FLNB, FLNA, PRKCB, GAD45G, PLA2G6, MAP3K14, GADD45A, MAP3K11, TNF, PPM1A, PPP3R1, GNG12, PPM1B, TNFRSF1A, RASGRP3, RASGRP4, MAP3K2, PLA2G12A, SOD1, MAPK31, RASGRP1, SOD2, PPP3CB, PPP3CC, NFATC4, PPP3CA, NFATC2, RAF1, MAPK11, TAB2, CDC25B, RPS6KA5, DUSP5, RPS6KA6, DUSP4, NRAS, RPS6KA4, DUSP2, MAPK12, RPS6KA1, RPS6KA2, MAPK14, DUSP9, DUSP8, CD14, DUSP6	2203	265	5738	1.42	1.93E-05	1.93E-06	1.25E-04
KEGG_PATHWAY	mmu04920:Adipocytokine signaling pathway	48	0.67	1.16E-07	PRKAG3, PPARG, TNF, NFKBIE, STK11, PRKAG1, NFKBIB, PRKAG2, NFKBIA, NFKB1, CAMKK1, CAMKK2, AKT1, TNFRSF1A, TNFRSF1B, ACSL1, SLC2A4, SLC2A1, PRKAA2, ACSL3, ACSL6, AKT3, ACSL5, AKT2, CPT1C, CPT1B, SOCS3, REL, RXRA, PRKAB2, RXRG, ADIPOR2, PRKAB1, ADIPOR1, ACACB, PCK2, PPARGC1A, IRS1, CPT1A, STAT3, TRADD, PTPN11, PRKQC, NPY, MAPK9, MAPK8, JAK2, IKKBK, NFKB1, PRKX, AKT1, PRKAR2B, CASP6, CASP3, PRKAR2A, MYD88, CASP9, CASP7, IL1RAP, CASP8, EXOG, CS2B8, IL1B, PIK3CA, AKT3, AKT2, PIK3CG, IRAK2, AIFM1, DFFA, RELB, PIK3CD, CYCS, FADD, TNFRSF10B, RIKP1, MAP3K14, NGF, BID, IL1R1, TNF, CSF2RB2, PPP3R1, NFKBIA, BCL2L1, IRAK4, IRAK3, TNFRSF1A, BCL2, PPP3CB, PPP3CC, PIK3R5, PPP3CA, TRPS3, ENDOD1, CAPN2, BIRC3, BIRC2, TRADD,	2203	67	5738	1.87	2.23E-05	2.03E-06	1.44E-04
KEGG_PATHWAY	mmu04210:Apoptosis	58	0.80	2.24E-07	CAPN1, TNFSF10, ENDOG, BAX, APAF1, IKKBK, IL3RA	2203	87	5738	1.74	4.33E-05	3.61E-06	2.79E-04
					UQCRC2, ATP1B1, UQCRC1, SLC9A6, ATP1B3, ATP1B2, CYC1, UQCRCF51, COX5A, UQCRCQ, COX5B, UQCRC10, UQCRC11, CACNG7, CACNG6, COX4I2, COX4I1, MYH7, CACNG1, COX6C, TNNT2, UQCRRH, UQCRR, FYO2D, MYL2, MYL3, COX7B, COX7C, CACNB1, CACNB3, COX7A2L, TPM2, TPM4, TPM3, COX6B1, COX6B2, CACNA2D1, ACTC1, COX7A2, COX7A1, COX8B, COX8A, ATP1A3, ATP1A2, ATP1A1, TNNA3, CACNA1S, CACNA2D4, ATP2A2, COX6A2, COX6A1, CACNA10, SLC9A1	2203	78	5738	1.77	6.42E-05	4.94E-06	4.14E-04
KEGG_PATHWAY	mmu00280:Valine, leucine and isoleucine degradation	35	0.49	9.64E-07	BGAT1, HSD17B10, ACADSB, BGAT2, EHHA0H, ECHS1, ACAT2, ACAT1, HIBADH, HADHA, ALDH3A2, HADHB, ALDH, MCCC2, MUT, IVD, MCCC1, MCEE, OXCT1, ACAD8, HADH, BKDHA, ACA4, ALDH6A1, ACADM, ACADS, BKDHB, DBT, ALDH1B1, DLD, AOX1, HIBCH, PCBA, PCCA, ALDH9A1	2203	46	5738	1.98	1.86E-04	1.33E-05	0.001200903
					NFKB1, BTK, AKT1, FOS, PIK3CA, PIK3AP1, AKT3, AKT2, PIK3CG, BCL10, LYN, REL, PIK3CD, HRAS1, PRKCB, CARD11, ILURB3, JUN, MAPK3, IFTM1, GRB2, NFKBIE, NFKBIB, PPP3R1, NFKBIA, RAC2, DAPP1, RASGRP3, RAC3, SOD1, SOD2, PPP3CB, CD22, PPP3CC, PIK3R5, NFATC4, PPP3CA, NIPPOD, NFATC2, BLNK, PTPN6, VAV3, MAP2K2, RAF1, MALTI, VAV2, VAV1, NRAS, FCGR2B, GSK3B, PLCG2, CD79B,	2203	80	5738	1.73	2.13E-04	1.42E-05	0.001375792
KEGG_PATHWAY	mmu04662:B cell receptor signaling pathway	53	0.73	1.10E-06	IKKBK	2203	80	5738	1.73	2.13E-04	1.42E-05	0.001375792
					FGF1B, PTGSD, PGF, PDGFA, MMP9, STAT5B, FGF13, MMP2, TGFBR1, TGFBR2, CUL2, WNT4, CDKN2B, SLC2A1, RALB, RALA, CSF3R, PIK3CA, RARA, RARB, PIK3CG, EGFR, BCR, REL, RXRA, PIK3CD, SKP2, RXRG, FADD, MECOM, CTNNA1, STK4, CTNNA3, HRAS1, VEGF8, CDC6, HF1A, PIAS3, JUN, MAPK3, VEGF9, PDGFR4, MAPK9, PIAS2, LAMC2, COX7C, CACNB1, CACNB3, COX7A2L, TPM2, TPM4, TPM3, BCL2L1, RIK1, LAMB2, RAC2, RAC1, ITGAV, FH1, EGF, RUNK1, TRAF3, TRAF4, CSF3R, FN1, TRPS3, DVL2, TC7F, EPAS1, MAP2K2, TGFBR1, TGFBR2, SMAD4, SMAD3, BIRCA2, ITGA3, HGF, DVL1, CDKN1A, LAMA4, HDACC2, ITGA6, HDACC1, PLCG2, IKKBK, FGF6, E2F1, E2F2, PPARG, NFKB1, NFKB2, GLI3, AKT1, ACVR1B, CCNE1, FOS, MAX, CASP3, CASP9, CASP8, RHOA, MYC, AKT3, CSF2RA, AKT2, PRKCA, CTBP1, AR, HSP90AA1, CYCS, CDK6, CDK4, CDK2, DAPK1, RADS1, PRKCB, SMO, CCND1, MDM2, WNT11, WNT9A, BID, CXSLB, PML, EGN2, DYT816, TCF7L2, TPM3, BCL2, SOD1, SOD2, PIK3R5, FLT3, HGF, CSF3A, FZD9, LGS, COL4A1, MSH3, MSH2, VHL, FLT3, CBL, FZD1, RAF1, IGF1, BIRC5, FZD2, APPR1, STAT1, BZDS, BIRC3, FZD4, BIRC2, RALGDS, FZD7, STAT3, FZD6, NRAS, RASSF5, HSP90B1, RASSF1,	2203	323	5738	1.34	2.35E-04	1.47E-05	0.001518548
KEGG_PATHWAY	mmu05200:Pathways in cancer	166	2.30	1.22E-06	GSK3B, BAX, ARAF, TCEB1	2203	323	5738	1.34	2.35E-04	1.47E-05	0.001518548
					PGF, PDGFA, VTN, MYL10, ACTG1, PIK3CA, PDGFR, EGFR, PIK3CG, ROCK1, ACTN4, ROCK2, PIK3CD, ACTN1, MYLK2, ACTN3, PPP1CB, HRAS1, VEGF8, JUN, VEGFA, MAPK3, PDGFR4, COL1A2, MAPK9, LAMC2, MAPK8, COL1A1, GAV1, MYL2, GRB2, ITGAB1, ITGB3, SRC, MYH9, DOKC1, LAMB2, RAC2, RAC3, ITGAV, ITGB7, ITGB6, EGF, FN1, SPP1, VAV3, ITGA3, MYL12B, ITGA4, HGF, VAV2, VAV1, KDR, ITGA9, LAMA4, ITGA6, ITGAS, ITGA7, RAP1B, TLN2, PIP5K1C, AKT1, ARHGAP5, PAK2, PAK4, RHOA, SHC1, ZYX, AKT3, AKT2, PRKCA, PARVG, FLNB, FLNA, VASP, PRKCB, CCND1, CCND3, CCND2, PARVA, TNC, COL3A1, SOD1, COMP, BCL2, SOD2, COL6A2, COL6A1, PIK3R5, TNN, THBS1, FIGF, THBS2, THBS3,	2203	198	5738	1.41	0.001467105	8.64E-05	0.009478696

KEGG_PATHWAY	mmu05212:Pancreatic cancer	47	0.65	9.20E-06	E2F1, E2F2, PGF, NFKB1, BCL2L1, TGFBI1, TGFBI2, AKT1, ACVR1B, RAC2, CASP9, RAC3, RALB, RALA, PIK3CA, PIK3RS, EGF, FIGF, AKT3, AKT2, PIK3CG, TRP53, EGFR, PLD1, RELA, ARHGEF6, TGFBR1, PIK3CD, TGFBR2, SMAD4, RAF1, BRCA2, SMAD3, CDK6, STAT1, CDK4, STAT3, RALGDS, RAD51, VEGFB, CCND1, ARAF, VEGFA, MAPK3, MAPK9, MAPK8, IKKB	2203	72	5738	1.70	0.001774079	9.86E-05	0.011463648
					TGFBI1, TGFBI2, AKT1, FOS, ACVR1B, CASP3, CASP9, PIK3CA, MYC, AKT3, AKT2, EGFR, PIK3CG, PIK3CD, CYCS, CCND1, JUN, MAPK3, PDGFRA, MAPK9, MAPK8, GRB2, TCF7L2, RAC2, RAC3, SOS1, BCL2, SOS2, PIK3RS, DVL2, FZD9, TRP53, TCF7, MSH3, MSH2, TGFBR1, TGFBR2, SMAD4, FZD1, RAF1, SMAD3, BIRC5, FZD2, FZD5, APPL1, FZD4, FZD7, RALGDS, FZD6, DVL1, BAX, GSK3B, ARAF							
KEGG_PATHWAY	mmu05210:Colorectal cancer	53	0.73	2.43E-05	E2F1, E2F2, GRB2, STAT5B, NFKBIA, NFKB1, BCL2L1, TGFBI1, TGFBI2, AKT1, ACVR1B, GAB2, SOS1, SOS2, PIK3CA, SHC1, PIK3RS, RUNX1, MYC, AKT3, AKT2, PIK3CG, TRP53, CTBP1, BCR, MAP2K2, RELA, TGFBR1, CBL, PIK3CD, TGFBR2, SMAD4, RAF1, SMAD3, CDK6, MECOM, CDK4, PTPN11, HRAS1, NRAS, CCND1, CDKN1A, HDAC2, HDAC1, ARAF, MAPK3, MDM2, IKKB	2203	86	5738	1.61	0.004670485	2.46E-04	0.030220506
KEGG_PATHWAY	mmu05220:Chronic myeloid leukemia	48	0.67	2.60E-05		2203	76	5738	1.65	0.005013764	2.51E-04	0.032446929

Table S2.F KEGG pathways significant at 168 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	18		0.65	4.47E-07 CCL2, FGR, NCF1, HCK, CCL9, CCL8, WAS, CCL7, CCL17, PRKCB, CCL12, CCR5, RAC2, CX3CR1, PIK3RS, XCL1, XCR1	129	182	5738	4.40	4.78E-05	4.78E-05	5.02E-04
KEGG_PATHWAY	mmu04670:Leukocyte transendothelial migration	14		0.50	1.93E-06 NCF2, NCF1, NCF4, ITGB2, PRKCB, VCAM1, CYBA, CYBB, EZR, RAC2, PLCG2, CLDN2, PIK3RS, RHOH	129	119	5738	5.23	2.06E-04	1.03E-04	0.002168346
KEGG_PATHWAY	mmu04650:Natural killer cell mediated cytotoxicity	13		0.47	1.46E-05 BID, FCGR4, ITGB2, NCR1, PRKCB, FCGR3, CD48, RAC2, PLCG2, FCER1G, PIK3RS, LCP2, TYROBP	129	122	5738	4.74	0.001563801	5.22E-04	0.016439609
KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	12		0.43	1.55E-05 C1QA, C1QB, C7, CD86, C4B, FCGR4, H2-DMB1, HIST1H4I, C1QC, FCGR1, IL10, FCGR3	129	103	5738	5.18	0.001652768	4.13E-04	0.017375573
KEGG_PATHWAY	mmu04060:Cytokine-cytokine receptor interaction	18		0.65	2.48E-05 CCL2, CSF2RB2, CCL9, CCL8, IL10, CCL7, CCL17, CCL12, CCR5, IL10RA, CCR2, CX3CR1, CSF2RB, IL2RG, IL12B, XCL1, XCR1, CSF2RA	129	244	5738	3.28	0.00265068	5.31E-04	0.027879105

Table S2.G KEGG pathways significant at 336 hours

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	18	2.36	7.85E-08	IBSP, TNC, COL3A1, ITGB5, ITGA4, COL5A3, COL5A2, SDC2, COL5A1, CD44, COL1A2, COL6A2, COL6A1, COL1A1, THBS2, THBS3, SPP1, FN1	254	83	5738	4.90	1.08E-05	1.08E-05	9.24E-05
KEGG_PATHWAY	mmu05416:Viral myocarditis	16	2.10	1.24E-05	H2-K1, ITGAL, MYH3, H2-D1, H2-DMB1, ITGB2, MYH7, H2-AB1, MYH8, CD86, H2-EB1, SGCD, H2-AA, MYH13, MYH14, ABL2	254	94	5738	3.85	0.001713391	8.57E-04	0.014623985
KEGG_PATHWAY	mmu04062:Chemokinesignalingpathway	23	3.01	1.34E-05	PARD3, CCL2, ADCY7, NCF1, STAT5B, CXCL9, CCL9, CCL8, GNG11, PF4, CCL6, CCL12, CCR5, ADCY9, TIAM1, CXCR4, GNG10, CXCL16, GSK3B, CCR2, SOS2, PAK1, SHC2	254	182	5738	2.85	0.001841954	6.14E-04	0.015722211
KEGG_PATHWAY	mmu04510:focal adhesion	24	3.15	1.64E-05	IBSP, FLT1, TNC, COL3A1, ITGB5, ITGA4, COL5A3, COL5A2, COL5A1, GSK3B, BCL2, SOS2, COL6A2, GRLF1, COL1A2, COL6A1, COL1A1, PAK1, EGF, SHC2, THBS2, THBS3, SPP1, FN1	254	198	5738	2.74	0.002258263	5.65E-04	0.019279342

Table S2.H KEGG pathways significant at 504 hours

Category	Term	Count	%	PValue	Genes
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	18	2.36	7.85E-08	IBSP, TNC, COL3A1, ITGB5, ITGA4, COL5A3, COL5A2, SDC2, COL5A1, CD44, COL1A2, COL6A2, COL6A1, COL1A1, THBS2, THBS3, SPP1, FN1
KEGG_PATHWAY	mmu05416:Viral myocarditis	16	2.10	1.24E-05	H2-K1, ITGAL, MYH3, H2-D1, H2-DMB1, ITGB2, MYH7, H2-AB1, MYH8, CD86, H2-EB1, SGCD, H2-AA, MYH13, MYH14, ABL2
KEGG_PATHWAY	mmu04062:Chemokine signaling pathway	23	3.01	1.34E-05	PARD3, CCL2, ADCY7, NCF1, STAT5B, CXCL9, CCL9, CCL8, GNG11, PF4, CCL6, CCL12, CCR5, ADCY9, TIAM1, CXCR4, GNG10, CXCL16, GSK3B, CCR2, SOS2, PAK1, SHC2
KEGG_PATHWAY	mmu04510:focal adhesion	24	3.15	1.64E-05	IBSP, FLT1, TNC, COL3A1, ITGB5, ITGA4, COL5A3, COL5A2, COL5A1, GSK3B, BCL2, SOS2, COL6A2, GRLF1, COL1A2, COL6A1, COL1A1, PAK1, EGF, SHC2, THBS2, THBS3, SPP1, FN1

Table S2.H KEGG pathways significant at 504 hours

List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
254	83	5738		4.90	1.08E-05	1.08E-05
254	94	5738		3.85	0.001713391	8.57E-04
254	182	5738		2.85	0.001841954	6.14E-04
254	198	5738		2.74	0.002258263	5.65E-04

Table S2.I KEGG pathways significant at 672 hours												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu04512:ECM-receptor interaction	17		2.51	7.58E-08 IBSP, TNC, COL3A1, ITGA4, COL5A2, SDC2, COL5A1, CD44, COMP, COL1A2, COL6A2, COL6A1, COL1A1, THBS2, COL11A1, THBS3, FN1	223	83	5738	5.27	1.08E-05	1.08E-05	8.96E-05
KEGG_PATHWAY	mmu04510:Focal adhesion	26		3.85	1.21E-07 IBSP, CAV2, CAV1, MYL2, TNC, COL3A1, BCL2, COMP, COL6A2, COL6A1, PAK1, EGF, COL11A1, THBS2, THBS3, FN1, VAV3, IGF1, ITGA4, COL5A2, COL5A1, PDGFRA, COL1A2, GRLF1, COL1A1, PARVA	223	198	5738	3.38	1.72E-05	8.62E-06	1.44E-04
KEGG_PATHWAY	mmu04610:Complement and coagulation cascades	15		2.22	7.70E-07 C3AR1, CFB, F13A1, SERPING1, C1S, C1QC, C1QA, C1QB, C1RA, CD55, F3, CFH, C2, CFB, PROS1	223	75	5738	5.15	1.09E-04	3.64E-05	9.10E-04

**Table S3.** Significant GO clusters identified from the 168h time point that were obtained from differentially expressed genes that were determined to contribute the largest variance at that time point.

Cluster 1: Enrichment Score: 11.54				
Annotation	GO Term	Gene Count	P-value	FDR
GOTERM_BP_FAT	vasculature development	85	5.20E-14	9.70E-11
GOTERM_BP_FAT	blood vessel development	83	1.00E-13	1.90E-10
GOTERM_BP_FAT	blood vessel morphogenesis	69	4.30E-12	8.00E-09
GOTERM_BP_FAT	angiogenesis	48	3.00E-09	5.60E-06
Cluster 2: Enrichment Score: 11.31				
Annotation	GO Term	Gene Count	P-value	FDR
GOTERM_CC_FAT	extracellular matrix	100	2.50E-14	3.60E-11
SP_PIR_KEYWORD	extracellular matrix	76	7.40E-14	1.10E-10
GOTERM_CC_FAT	proteinaceous extracellular m	96	9.40E-14	1.40E-10
GOTERM_CC_FAT	extracellular region part	179	1.10E-09	1.60E-06
GOTERM_CC_FAT	extracellular matrix part	37	1.50E-08	2.20E-05
Cluster 3: Enrichment Score: 9.38				
Annotation	GO Term	Gene Count	P-value	FDR
KEGG_PATHWAY	lysosome	53	2.40E-12	3.00E-09
SP_PIR_KEYWORD	lysosome	52	5.60E-10	8.30E-07
GOTERM_CC_FAT	lysosome	60	1.00E-09	1.50E-06
GOTERM_CC_FAT	lytic vacuole	60	1.30E-09	1.90E-06
GOTERM_CC_FAT	vacuole	64	6.80E-09	9.90E-06
Cluster 4: Enrichment Score: 7.85				
Annotation	GO Term	Gene Count	P-value	FDR
GOTERM_BP_FAT	vesicle-mediated transport	121	2.70E-10	5.00E-07
GOTERM_BP_FAT	membrane invagination	61	2.10E-09	3.90E-06
GOTERM_BP_FAT	endocytosis	61	2.10E-09	3.90E-06
GOTERM_BP_FAT	membrane organization	76	3.10E-08	5.70E-05
SP_PIR_KEYWORD	endocytosis	31	1.60E-05	2.40E-02
Cluster 5: Enrichment Score: 7.18				
Annotation	GO Term	Gene Count	P-value	FDR
GOTERM_BP_FAT	actin filament-based process	61	1.10E-10	2.00E-07
GOTERM_BP_FAT	actin cytoskeleton organization	57	5.60E-10	1.00E-06
GOTERM_BP_FAT	actin filament organization	23	6.70E-06	1.20E-02
GOTERM_BP_FAT	cytoskeleton organization	76	4.80E-05	8.80E-02